

SEQUENCE LISTING

<110> McCall, Catherine A.
Hunter, Shirley Wu
Weber, Eric R.

<120> NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
AND USES THEREOF

<130> AL-2-C4

<140> not yet assigned

<141> 2000-09-14

<150> 09/292,225

<151> 1999-04-15

<150> 60/098,909

<151> 1998-09-02

<150> 60/085,295

<151> 1998-05-13

<150> 60/098,565

<151> 1998-04-17

<150> 09/062,013

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<160> 57

<170> PatentIn Ver. 2.1

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<212> PRT

<213> Dermatophagoides farinae

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Tyr Lys Arg Pro
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<220>

<223> At locations 3 and 7, Xaa = any amino acid

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Leu Asn Asn Gly Ala Thr Arg
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<220>
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Glu

<210> 11
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<213> Dermatophagoides farinae

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Gly Val

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Asp Pro Ala Lys Gly Met Ser Pro Pro Gly Phe Ile Val Gly Glu Glu
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Gly Val Leu Ser
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<210> 14
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 <212> DNA
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<220>
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 Met Asn Ala Ser Ile Lys Arg Asp His Asn Asp Tyr Ser Lys Asn Pro
 20 25 30
 atg aga att gtt tgt tat gtt gga aca tgg tcc gta tat cat aaa gtt 144
 Met Arg Ile Val Cys Tyr Val Gly Thr Trp Ser Val Tyr His Lys Val
 35 40 45
 gat cca tac act atc gaa gat att gat cca ttc aag tgt aca cat tta 192
 Asp Pro Tyr Thr Ile Glu Asp Ile Asp Pro Phe Lys Cys Thr His Leu
 50 55 60
 atg tat ggt ttc gct aaa att gat gaa tac aaa tac aca att caa gtt 240
 Met Tyr Gly Phe Ala Lys Ile Asp Glu Tyr Lys Tyr Thr Ile Gln Val
 65 70 75 80
 ttc gat cct tac caa gat gat aac cat aac tca tgg gaa aaa cgt ggt 288
 Phe Asp Pro Tyr Gln Asp Asp Asn His Asn Ser Trp Glu Lys Arg Gly
 85 90 95
 tat gaa cgt ttc aac aac ttg cga ttg aag aat cca gaa tta acc acc 336
 Tyr Glu Arg Phe Asn Asn Leu Arg Leu Lys Asn Pro Glu Leu Thr Thr
 100 105 110
 atg att tca ctt ggt ggt tgg tat gaa ggc tcg gaa aaa tat tcc gat 384
 Met Ile Ser Leu Gly Gly Trp Tyr Glu Gly Ser Glu Lys Tyr Ser Asp
 115 120 125

001150-000000

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| Leu Cys Gln Leu Phe Gln Lys Glu Glu Trp His Ile Gln Tyr Asp Glu | |
| 325 330 335 | |
| tat tac aat gct cca tat ggt tac aat gat aaa atc tgg gtc ggt tac | 1056 |
| Tyr Tyr Asn Ala Pro Tyr Gly Tyr Asn Asp Lys Ile Trp Val Gly Tyr | |
| 340 345 350 | |
| gat gat ctg gcc agt ata tca tgc aag ttg gct ttc ctg aaa gaa tta | 1104 |
| Asp Asp Leu Ala Ser Ile Ser Cys Lys Leu Ala Phe Leu Lys Glu Leu | |
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| ggc gtt tct ggt gtc atg gtt tgg tca ttg gaa aat gat gat ttc aaa | 1152 |
| Gly Val Ser Gly Val Met Val Trp Ser Leu Glu Asn Asp Asp Phe Lys | |
| 370 375 380 | |
| ggt cac tgc gga ccg aaa aat cca ttg ttg aac aaa gtt cat aat atg | 1200 |
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| 385 390 395 400 | |
| att aat ggc gat gaa aag aac tct ttc gaa tgc att ttg ggt cca agt | 1248 |
| Ile Asn Gly Asp Glu Lys Asn Ser Phe Glu Cys Ile Leu Gly Pro Ser | |
| 405 410 415 | |
| aca acg aca cca act cca acg acg aca ccc aca acc ccg act aca acg | 1296 |
| Thr Thr Thr Pro Thr Pro Thr Thr Thr Pro Thr Thr Pro Thr Thr Thr | |
| 420 425 430 | |
| cca aca act cct tct ccc acc acc ccg aca aca acc cct tct ccc acc | 1344 |
| Pro Thr Thr Pro Ser Pro Thr Thr Pro Thr Thr Pro Ser Pro Thr | |
| 435 440 445 | |
| acc ccg aca aca acc cct tct ccc acc aca ccg aca aca act cct tct | 1392 |
| Thr Pro Thr Thr Thr Pro Ser Pro Thr Thr Pro Thr Thr Thr Pro Ser | |
| 450 455 460 | |
| ccc acc aca cca aca cca aca aca cca aca cca gcc cct aca aca tcg | 1440 |
| Pro Thr Thr Pro Thr Pro Thr Thr Pro Thr Pro Ala Pro Thr Thr Ser | |
| 465 470 475 480 | |
| aca cct tcg cca acc acg acc gaa cac aca agc gaa aca cca aaa tat | 1488 |
| Thr Pro Ser Pro Thr Thr Thr Glu His Thr Ser Glu Thr Pro Lys Tyr | |
| 485 490 495 | |
| aca acc tat gtc gat gga cat ctt atc aaa tgt tac aag gaa ggt gat | 1536 |
| Thr Thr Tyr Val Asp Gly His Leu Ile Lys Cys Tyr Lys Glu Gly Asp | |
| 500 505 510 | |

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Asn | Pro | Thr | Tyr | Arg | Gln | Gln | Phe | Ile | Gln | Ser | Val | Leu | 130 | 135 | 140 | |
| Asp | Phe | Leu | Gln | Glu | Tyr | Lys | Phe | Asp | Gly | Leu | Asp | Leu | Asp | Trp | Glu | 145 | 150 | 155 | 160 |
| Tyr | Pro | Gly | Ser | Arg | Leu | Gly | Asn | Pro | Lys | Ile | Asp | Lys | Gln | Asn | Tyr | 165 | 170 | 175 | |
| Leu | Ala | Leu | Val | Arg | Glu | Leu | Lys | Asp | Ala | Phe | Glu | Pro | His | Gly | Tyr | 180 | 185 | 190 | |
| Leu | Leu | Thr | Ala | Ala | Val | Ser | Pro | Gly | Lys | Asp | Lys | Ile | Asp | Arg | Ala | 195 | 200 | 205 | |
| Tyr | Asp | Ile | Lys | Glu | Leu | Asn | Lys | Leu | Phe | Asp | Trp | Met | Asn | Val | Met | 210 | 215 | 220 | |
| Thr | Tyr | Asp | Tyr | His | Gly | Gly | Trp | Glu | Asn | Phe | Tyr | Gly | His | Asn | Ala | 225 | 230 | 235 | 240 |
| Pro | Leu | Tyr | Lys | Arg | Pro | Asp | Glu | Thr | Asp | Glu | Leu | His | Thr | Tyr | Phe | 245 | 250 | 255 | |
| Asn | Val | Asn | Tyr | Thr | Met | His | Tyr | Tyr | Leu | Asn | Asn | Gly | Ala | Thr | Arg | 260 | 265 | 270 | |
| Asp | Lys | Leu | Val | Met | Gly | Val | Pro | Phe | Tyr | Gly | Arg | Ala | Trp | Ser | Ile | 275 | 280 | 285 | |
| Glu | Asp | Arg | Ser | Lys | Leu | Lys | Leu | Gly | Asp | Pro | Ala | Lys | Gly | Met | Ser | 290 | 295 | 300 | |
| Pro | Pro | Gly | Phe | Ile | Ser | Gly | Glu | Glu | Gly | Val | Leu | Ser | Tyr | Ile | Glu | 305 | 310 | 315 | 320 |
| Leu | Cys | Gln | Leu | Phe | Gln | Lys | Glu | Glu | Trp | His | Ile | Gln | Tyr | Asp | Glu | 325 | 330 | 335 | |
| Tyr | Tyr | Asn | Ala | Pro | Tyr | Gly | Tyr | Asn | Asp | Lys | Ile | Trp | Val | Gly | Tyr | 340 | 345 | 350 | |
| Asp | Asp | Leu | Ala | Ser | Ile | Ser | Cys | Lys | Leu | Ala | Phe | Leu | Lys | Glu | Leu | 355 | 360 | 365 | |
| Gly | Val | Ser | Gly | Val | Met | Val | Trp | Ser | Leu | Glu | Asn | Asp | Asp | Phe | Lys | 370 | 375 | 380 | |

Gly His Cys Gly Pro Lys Asn Pro Leu Leu Asn Lys Val His Asn Met
385 390 395 400

Ile Asn Gly Asp Glu Lys Asn Ser Phe Glu Cys Ile Leu Gly Pro Ser
405 410 415

Thr Thr Thr Pro Thr Pro Thr Thr Thr Pro Thr Thr Pro Thr Thr Thr
420 425 430

Pro Thr Thr Pro Ser Pro Thr Thr Pro Thr Thr Thr Pro Ser Pro Thr
435 440 445

Thr Pro Thr Thr Thr Pro Ser Pro Thr Thr Pro Thr Thr Thr Pro Ser
450 455 460

Pro Thr Thr Pro Thr Pro Thr Thr Pro Thr Pro Ala Pro Thr Thr Ser
465 470 475 480

Thr Pro Ser Pro Thr Thr Thr Glu His Thr Ser Glu Thr Pro Lys Tyr
485 490 495

Thr Thr Tyr Val Asp Gly His Leu Ile Lys Cys Tyr Lys Glu Gly Asp
500 505 510

Ile Pro His Pro Thr Asn Ile His Lys Tyr Leu Val Cys Glu Phe Val
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aatagtcccc ggtggacagg gcataatatg aaccaccag ccaccattaa caaattcaca 180
gaccaaatat ttgtgtatat tgggtggatg tgggatatca ccttccttgt aacatttgat 240
aagatgtcca tcgacatagg ttgtatatatt tgggtgtttcg cttgtgtgtt cggtcgtggt 300
tggcgaaggt gtcgatgttg taggggctgg tgttggtgtt gttggtgttg gtgtggtggg 360
agaaggagtt gttgtcgggtg tgggtgggaga aggggttgtt gtcgggggtg tgggagaagg 420

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atcgccatta atcatattat gaactttgtt caacaatgga tttttcggtc cgcagtgacc 600
tttgaaatca tcattttcca atgaccaaac catgacacca gaaacgccta attctttcag 660
gaaagccaac ttgcatgata tactggccag atcatcgtaa ccgaccaga ttttatcatt 720
gtaaccatat ggagcattgt aatattcatt gtattggata tgccattctt ctttttgaaa 780
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atagtgcatt gtgtagtgtg cattgaagta agtgtgcaac tcatcagttt catctggtcg 1020
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catgacattc atccaatcga acaatttgtt caattctttg atatcataag ctcggtcgat 1140
tttgtcttta cctggtgata ctgcagcagt caacaagtag ccatgagggt caaaagcgtc 1200
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tacggaccat gttccaacat aacaaacaat tctcatcgga tttttcgaat aatcattatg 1680
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<210> 17
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<220>
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 <222> (1)..(1665)

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atg aat gca tcc atc aaa cga gat cat aat gat tat tcg aaa aat ccg 96
Met Asn Ala Ser Ile Lys Arg Asp His Asn Asp Tyr Ser Lys Asn Pro
      20             25            30

atg aga att gtt tgt tat gtt gga aca tgg tcc gta tat cat aaa gtt 144
Met Arg Ile Val Cys Tyr Val Gly Thr Trp Ser Val Tyr His Lys Val
      35             40            45

gat cca tac act atc gaa gat att gat cca ttc aag tgt aca cat tta 192

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| Asp | Pro | Tyr | Thr | Ile | Glu | Asp | Ile | Asp | Pro | Phe | Lys | Cys | Thr | His | Leu | |
| 50 | | | | | | 55 | | | | | 60 | | | | | |
| atg | tat | ggg | ttc | gct | aaa | att | gat | gaa | tac | aaa | tac | aca | att | caa | gtt | 240 |
| Met | Tyr | Gly | Phe | Ala | Lys | Ile | Asp | Glu | Tyr | Lys | Tyr | Thr | Ile | Gln | Val | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| ttc | gat | cct | tac | caa | gat | gat | aac | cat | aac | tca | tgg | gaa | aaa | cgt | ggg | 288 |
| Phe | Asp | Pro | Tyr | Gln | Asp | Asp | Asn | His | Asn | Ser | Trp | Glu | Lys | Arg | Gly | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| tat | gaa | cgt | ttc | aac | aac | ttg | cga | ttg | aag | aat | cca | gaa | tta | acc | acc | 336 |
| Tyr | Glu | Arg | Phe | Asn | Asn | Leu | Arg | Leu | Lys | Asn | Pro | Glu | Leu | Thr | Thr | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
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| Met | Ile | Ser | Leu | Gly | Gly | Trp | Tyr | Glu | Gly | Ser | Glu | Lys | Tyr | Ser | Asp | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| atg | gct | gca | aat | cca | aca | tat | cgt | caa | caa | ttc | ata | caa | tca | gtt | ttg | 432 |
| Met | Ala | Ala | Asn | Pro | Thr | Tyr | Arg | Gln | Gln | Phe | Ile | Gln | Ser | Val | Leu | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| gac | ttt | ttg | caa | gaa | tac | aag | ttc | gac | ggg | cta | gat | ttg | gat | tgg | gag | 480 |
| Asp | Phe | Leu | Gln | Glu | Tyr | Lys | Phe | Asp | Gly | Leu | Asp | Leu | Asp | Trp | Glu | |
| 145 | | | | 150 | | | | | 155 | | | | | 160 | | |
| tat | cct | gga | tct | cga | ttg | ggg | aac | ccg | aaa | atc | gat | aaa | caa | aac | tat | 528 |
| Tyr | Pro | Gly | Ser | Arg | Leu | Gly | Asn | Pro | Lys | Ile | Asp | Lys | Gln | Asn | Tyr | |
| | | | 165 | | | | | | 170 | | | | | 175 | | |
| ttg | gct | ttg | gtt | aga | gaa | ctt | aaa | gac | gct | ttt | gaa | cct | cat | ggc | tac | 576 |
| Leu | Ala | Leu | Val | Arg | Glu | Leu | Lys | Asp | Ala | Phe | Glu | Pro | His | Gly | Tyr | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| ttg | ttg | act | gct | gca | gta | tca | cca | ggg | aaa | gac | aaa | atc | gac | cga | gct | 624 |
| Leu | Leu | Thr | Ala | Ala | Val | Ser | Pro | Gly | Lys | Asp | Lys | Ile | Asp | Arg | Ala | |
| | | 195 | | | | | | 200 | | | | 205 | | | | |
| tat | gat | atc | aaa | gaa | ttg | aac | aaa | ttg | ttc | gat | tgg | atg | aat | gtc | atg | 672 |
| Tyr | Asp | Ile | Lys | Glu | Leu | Asn | Lys | Leu | Phe | Asp | Trp | Met | Asn | Val | Met | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| aca | tat | gat | tac | cac | ggg | gga | tgg | gaa | aac | ttt | tac | ggg | cac | aat | gct | 720 |
| Thr | Tyr | Asp | Tyr | His | Gly | Gly | Trp | Glu | Asn | Phe | Tyr | Gly | His | Asn | Ala | |
| 225 | | | | 230 | | | | | | 235 | | | | 240 | | |
| ccg | ttg | tat | aaa | cga | cca | gat | gaa | act | gat | gag | ttg | cac | act | tac | ttc | 768 |

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Pro | Leu | Tyr | Lys | Arg | Pro | Asp | Glu | Thr | Asp | Glu | Leu | His | Thr | Tyr | Phe | | |
| | | | | 245 | | | | | 250 | | | | | 255 | | | |
| aat | gtc | aac | tac | acc | atg | cac | tat | tat | ttg | aac | aat | ggc | gcc | acc | aga | 816 | |
| Asn | Val | Asn | Tyr | Thr | Met | His | Tyr | Tyr | Leu | Asn | Asn | Gly | Ala | Thr | Arg | | |
| | | | 260 | | | | | 265 | | | | | 270 | | | | |
| gac | aaa | ttg | gta | atg | ggc | gtt | cca | ttc | tat | ggc | cgt | gct | tgg | agc | att | 864 | |
| Asp | Lys | Leu | Val | Met | Gly | Val | Pro | Phe | Tyr | Gly | Arg | Ala | Trp | Ser | Ile | | |
| | | 275 | | | | | 280 | | | | | 285 | | | | | |
| gaa | gat | cga | agc | aaa | ctc | aaa | ctt | gga | gat | cca | gcc | aaa | ggc | atg | tcg | 912 | |
| Glu | Asp | Arg | Ser | Lys | Leu | Lys | Leu | Gly | Asp | Pro | Ala | Lys | Gly | Met | Ser | | |
| | 290 | | | | | 295 | | | | | 300 | | | | | | |
| ccc | cca | ggc | ttc | att | tct | ggc | gaa | gaa | ggc | gtc | ctc | tca | tat | ata | gaa | 960 | |
| Pro | Pro | Gly | Phe | Ile | Ser | Gly | Glu | Glu | Gly | Val | Leu | Ser | Tyr | Ile | Glu | | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | | |
| ttg | tgt | caa | ttg | ttt | caa | aaa | gaa | gaa | tgg | cat | atc | caa | tac | gat | gaa | 1008 | |
| Leu | Cys | Gln | Leu | Phe | Gln | Lys | Glu | Glu | Trp | His | Ile | Gln | Tyr | Asp | Glu | | |
| | | | | 325 | | | | | 330 | | | | | 335 | | | |
| tat | tac | aat | gct | cca | tat | ggc | tac | aat | gat | aaa | atc | tgg | gtc | ggc | tac | 1056 | |
| Tyr | Tyr | Asn | Ala | Pro | Tyr | Gly | Tyr | Asn | Asp | Lys | Ile | Trp | Val | Gly | Tyr | | |
| | | | 340 | | | | | 345 | | | | | 350 | | | | |
| gat | gat | ctg | gcc | agt | ata | tca | tgc | aag | ttg | gct | ttc | ctg | aaa | gaa | tta | 1104 | |
| Asp | Asp | Leu | Ala | Ser | Ile | Ser | Cys | Lys | Leu | Ala | Phe | Leu | Lys | Glu | Leu | | |
| | | 355 | | | | | 360 | | | | | 365 | | | | | |
| ggc | gtt | tct | ggc | gtc | atg | gtt | tgg | tca | ttg | gaa | aat | gat | gat | ttc | aaa | 1152 | |
| Gly | Val | Ser | Gly | Val | Met | Val | Trp | Ser | Leu | Glu | Asn | Asp | Asp | Phe | Lys | | |
| | 370 | | | | | 375 | | | | | 380 | | | | | | |
| ggc | cac | tgc | gga | ccg | aaa | aat | cca | ttg | ttg | aac | aaa | gtt | cat | aat | atg | 1200 | |
| Gly | His | Cys | Gly | Pro | Lys | Asn | Pro | Leu | Leu | Asn | Lys | Val | His | Asn | Met | | |
| | 385 | | | | 390 | | | | | 395 | | | | | 400 | | |
| att | aat | ggc | gat | gaa | aag | aac | tct | ttc | gaa | tgc | att | ttg | ggc | cca | agt | 1248 | |
| Ile | Asn | Gly | Asp | Glu | Lys | Asn | Ser | Phe | Glu | Cys | Ile | Leu | Gly | Pro | Ser | | |
| | | | | 405 | | | | | 410 | | | | | 415 | | | |
| aca | acg | aca | cca | act | cca | acg | acg | aca | ccc | aca | acc | ccg | act | aca | acg | 1296 | |
| Thr | Thr | Thr | Pro | Thr | Pro | Thr | Thr | Thr | Pro | Thr | Thr | Pro | Thr | Thr | Thr | | |
| | | | 420 | | | | | 425 | | | | | 430 | | | | |
| cca | aca | act | cct | tct | ccc | acc | acc | ccg | aca | aca | acc | cct | tct | ccc | acc | 1344 | |

| | |
|---|------|
| Pro Thr Thr Pro Ser Pro Thr Thr Pro Thr Thr Thr Pro Ser Pro Thr | |
| 435 440 445 | |
| acc ccg aca aca acc cct tct ccc acc aca ccg aca aca act cct tct | 1392 |
| Thr Pro Thr Thr Thr Pro Ser Pro Thr Thr Pro Thr Thr Thr Pro Ser | |
| 450 455 460 | |
| ccc acc aca cca aca cca aca aca cca aca cca gcc cct aca aca tcg | 1440 |
| Pro Thr Thr Pro Thr Pro Thr Thr Pro Thr Pro Ala Pro Thr Thr Ser | |
| 465 470 475 480 | |
| aca cct tcg cca acc acg acc gaa cac aca agc gaa aca cca aaa tat | 1488 |
| Thr Pro Ser Pro Thr Thr Thr Glu His Thr Ser Glu Thr Pro Lys Tyr | |
| 485 490 495 | |
| aca acc tat gtc gat gga cat ctt atc aaa tgt tac aag gaa ggt gat | 1536 |
| Thr Thr Tyr Val Asp Gly His Leu Ile Lys Cys Tyr Lys Glu Gly Asp | |
| 500 505 510 | |
| atc cca cat cca acc aat ata cac aaa tat ttg gtc tgt gaa ttt gtt | 1584 |
| Ile Pro His Pro Thr Asn Ile His Lys Tyr Leu Val Cys Glu Phe Val | |
| 515 520 525 | |
| aat ggt ggc tgg tgg gtt cat att atg ccc tgt cca ccg ggc act att | 1632 |
| Asn Gly Gly Trp Trp Val His Ile Met Pro Cys Pro Pro Gly Thr Ile | |
| 530 535 540 | |
| tgg tgt caa gaa aaa ttg act tgt ata ggc gaa | 1665 |
| Trp Cys Gln Glu Lys Leu Thr Cys Ile Gly Glu | |
| 545 550 555 | |
| <210> 18 | |
| <211> 555 | |
| <212> PRT | |
| <213> Dermatophagoides farinae | |
| <400> 18 | |
| Met Lys Thr Ile Tyr Ala Ile Leu Ser Ile Met Ala Cys Ile Gly Leu | |
| 1 5 10 15 | |
| Met Asn Ala Ser Ile Lys Arg Asp His Asn Asp Tyr Ser Lys Asn Pro | |
| 20 25 30 | |
| Met Arg Ile Val Cys Tyr Val Gly Thr Trp Ser Val Tyr His Lys Val | |
| 35 40 45 | |
| Asp Pro Tyr Thr Ile Glu Asp Ile Asp Pro Phe Lys Cys Thr His Leu | |

| | | |
|---|---------|---------|
| 50 | 55 | 60 |
| Met Tyr Gly Phe Ala Lys Ile Asp Glu Tyr Lys Tyr Thr Ile Gln Val | | |
| 65 | 70 | 75 80 |
| Phe Asp Pro Tyr Gln Asp Asp Asn His Asn Ser Trp Glu Lys Arg Gly | | |
| | 85 90 | 95 |
| Tyr Glu Arg Phe Asn Asn Leu Arg Leu Lys Asn Pro Glu Leu Thr Thr | | |
| | 100 105 | 110 |
| Met Ile Ser Leu Gly Gly Trp Tyr Glu Gly Ser Glu Lys Tyr Ser Asp | | |
| | 115 120 | 125 |
| Met Ala Ala Asn Pro Thr Tyr Arg Gln Gln Phe Ile Gln Ser Val Leu | | |
| | 130 135 | 140 |
| Asp Phe Leu Gln Glu Tyr Lys Phe Asp Gly Leu Asp Leu Asp Trp Glu | | |
| | 145 150 | 155 160 |
| Tyr Pro Gly Ser Arg Leu Gly Asn Pro Lys Ile Asp Lys Gln Asn Tyr | | |
| | 165 170 | 175 |
| Leu Ala Leu Val Arg Glu Leu Lys Asp Ala Phe Glu Pro His Gly Tyr | | |
| | 180 185 | 190 |
| Leu Leu Thr Ala Ala Val Ser Pro Gly Lys Asp Lys Ile Asp Arg Ala | | |
| | 195 200 | 205 |
| Tyr Asp Ile Lys Glu Leu Asn Lys Leu Phe Asp Trp Met Asn Val Met | | |
| | 210 215 | 220 |
| Thr Tyr Asp Tyr His Gly Gly Trp Glu Asn Phe Tyr Gly His Asn Ala | | |
| | 225 230 | 235 240 |
| Pro Leu Tyr Lys Arg Pro Asp Glu Thr Asp Glu Leu His Thr Tyr Phe | | |
| | 245 250 | 255 |
| Asn Val Asn Tyr Thr Met His Tyr Tyr Leu Asn Asn Gly Ala Thr Arg | | |
| | 260 265 | 270 |
| Asp Lys Leu Val Met Gly Val Pro Phe Tyr Gly Arg Ala Trp Ser Ile | | |
| | 275 280 | 285 |
| Glu Asp Arg Ser Lys Leu Lys Leu Gly Asp Pro Ala Lys Gly Met Ser | | |
| | 290 295 | 300 |
| Pro Pro Gly Phe Ile Ser Gly Glu Glu Gly Val Leu Ser Tyr Ile Glu | | |

| | | | | | | |
|---|-----|-----|-----|-----|-----|-----|
| 305 | | 310 | | 315 | | 320 |
| Leu Cys Gln Leu Phe Gln Lys Glu Glu Trp His Ile Gln Tyr Asp Glu | | | | | | |
| | 325 | | 330 | | 335 | |
| Tyr Tyr Asn Ala Pro Tyr Gly Tyr Asn Asp Lys Ile Trp Val Gly Tyr | | | | | | |
| | 340 | | 345 | | 350 | |
| Asp Asp Leu Ala Ser Ile Ser Cys Lys Leu Ala Phe Leu Lys Glu Leu | | | | | | |
| | 355 | | 360 | | 365 | |
| Gly Val Ser Gly Val Met Val Trp Ser Leu Glu Asn Asp Asp Phe Lys | | | | | | |
| | 370 | | 375 | | 380 | |
| Gly His Cys Gly Pro Lys Asn Pro Leu Leu Asn Lys Val His Asn Met | | | | | | |
| | 385 | | 390 | | 395 | 400 |
| Ile Asn Gly Asp Glu Lys Asn Ser Phe Glu Cys Ile Leu Gly Pro Ser | | | | | | |
| | 405 | | 410 | | 415 | |
| Thr Thr Thr Pro Thr Pro Thr Thr Thr Pro Thr Thr Pro Thr Thr Thr | | | | | | |
| | 420 | | 425 | | 430 | |
| Pro Thr Thr Pro Ser Pro Thr Thr Pro Thr Thr Thr Pro Ser Pro Thr | | | | | | |
| | 435 | | 440 | | 445 | |
| Thr Pro Thr Thr Thr Pro Ser Pro Thr Thr Pro Thr Thr Thr Pro Ser | | | | | | |
| | 450 | | 455 | | 460 | |
| Pro Thr Thr Pro Thr Pro Thr Thr Pro Thr Pro Ala Pro Thr Thr Ser | | | | | | |
| | 465 | | 470 | | 475 | 480 |
| Thr Pro Ser Pro Thr Thr Thr Glu His Thr Ser Glu Thr Pro Lys Tyr | | | | | | |
| | 485 | | 490 | | 495 | |
| Thr Thr Tyr Val Asp Gly His Leu Ile Lys Cys Tyr Lys Glu Gly Asp | | | | | | |
| | 500 | | 505 | | 510 | |
| Ile Pro His Pro Thr Asn Ile His Lys Tyr Leu Val Cys Glu Phe Val | | | | | | |
| | 515 | | 520 | | 525 | |
| Asn Gly Gly Trp Trp Val His Ile Met Pro Cys Pro Pro Gly Thr Ile | | | | | | |
| | 530 | | 535 | | 540 | |
| Trp Cys Gln Glu Lys Leu Thr Cys Ile Gly Glu | | | | | | |
| | 545 | | 550 | | 555 | |

<210> 19
 <211> 1665
 <212> DNA
 <213> Dermatophagoides farinae

<400> 19
 ttcgcctata caagtcaatt tttcttgaca ccaaatagtg cccggtggac agggcataat 60
 atgaaccac cagccaccat taacaaattc acagaccaa tatttgtgta tattggttgg 120
 atgtgggata tcaccttctt tgtaacattt gataagatgt ccatcgacat aggttgtata 180
 ttttgggtgt tcgcttgtgt gttcgggtcgt ggttggcgaa ggtgtcgatg ttgtaggggc 240
 tgggtgttgg gttgttgggt ttggtgtggt gggagaagga gttgttgtcg gtgtgggtggg 300
 agaaggggtt gttgtcgggg tgggtgggaga aggggttgtt gtcgggggtgg tgggagaagg 360
 agttgttggc gttgttagtcg gggttgtggg tgtcgtcgtt ggagttgggtg tcgttgtact 420
 tggacccaaa atgcattcga aagagttctt ttcacgcca ttaatcatat tatgaacttt 480
 gttcaacaat ggatttttcg gtccgcagtg acctttgaaa tcatcatttt ccaatgacca 540
 aaccatgaca ccagaaacgc ctaattcttt caggaaagcc aacttgcattg atatactggc 600
 cagatcatcg taaccgaccc agattttatc attgtaacca tatggagcat tgtaatatctc 660
 atcgtattgg atatgccatt cttctttttg aaacaattga cacaattcta tatatgagag 720
 gacaccttct tcaccagaaa tgaaacctgg gggcgacatg ctttgggtg gatctccaag 780
 tttgagtttg cttcgatctt caatgctcca agcacggcca tagaatggaa caccattac 840
 caatttgtct ctggtggcac cattgttcaa ataatagtgc atggtgtagt tgacattgaa 900
 gtaagtgtgc aactcatcag tttcatctgg tcgtttatac aacggagcat tgtgaccgta 960
 aaagttttcc catccaccgt ggtaatcata tgcacatgaca ttcacccaat cgaacaattt 1020
 gttcaattct ttgatatacat aagctcggtc gattttgtct ttacctggtg atactgcagc 1080
 agtcaacaag tagccatgag gttcaaaagc gtctttaagt tctctaacca aagccaaata 1140
 gttttgttta tcgattttcg ggtaaccaa tcgagatcca ggatactccc aatccaaatc 1200
 tagaccgtcg aacttgtatt cttgcaaaaa gtccaaaact gattgtatga attgttgacg 1260
 atatgttggg tttgcagcca tatcggaata tttttccgag cttcatacc aaccaccaag 1320
 tgaaatcatg gtggttaatt ctggattctt caatcgcaag ttgttgaaac gttcataacc 1380
 acgtttttcc catgagttat gggtatcatc ttggtaagga tcgaaaactt gaattgtgta 1440
 tttgtattca tcaatttttag cgaaaccata cattaaatgt gtacacttga atggatcaat 1500
 atcttcgata gtgtatggat caactttatg atatacggac catgttccaa cataacaaac 1560
 aattctcatc ggatttttcg aataatcatt atgatctcgt ttgatggatg cattcataag 1620
 gccaatgcag gccataatac taagtattgc atatatgggtt ttcatt 1665

<210> 20
 <211> 1608
 <212> DNA
 <213> Dermatophagoides farinae

<220>
 <221> CDS
 <222> (1)..(1608)

<400> 20
 tcc atc aaa cga gat cat aat gat tat tcg aaa aat ccg atg aga att 48

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ile | Lys | Arg | Asp | His | Asn | Asp | Tyr | Ser | Lys | Asn | Pro | Met | Arg | Ile | |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | | |
| ggt | tgt | tat | ggt | gga | aca | tgg | tcc | gta | tat | cat | aaa | ggt | gat | cca | tac | 96 |
| Val | Cys | Tyr | Val | Gly | Thr | Trp | Ser | Val | Tyr | His | Lys | Val | Asp | Pro | Tyr | |
| | | | 20 | | | | 25 | | | | | 30 | | | | |
| act | atc | gaa | gat | att | gat | cca | ttc | aag | tgt | aca | cat | tta | atg | tat | ggt | 144 |
| Thr | Ile | Glu | Asp | Ile | Asp | Pro | Phe | Lys | Cys | Thr | His | Leu | Met | Tyr | Gly | |
| | | | 35 | | | | 40 | | | | | 45 | | | | |
| ttc | gct | aaa | att | gat | gaa | tac | aaa | tac | aca | att | caa | ggt | ttc | gat | cct | 192 |
| Phe | Ala | Lys | Ile | Asp | Glu | Tyr | Lys | Tyr | Thr | Ile | Gln | Val | Phe | Asp | Pro | |
| | | 50 | | | | | 55 | | | | 60 | | | | | |
| tac | caa | gat | gat | aac | cat | aac | tca | tgg | gaa | aaa | cgt | ggt | tat | gaa | cgt | 240 |
| Tyr | Gln | Asp | Asp | Asn | His | Asn | Ser | Trp | Glu | Lys | Arg | Gly | Tyr | Glu | Arg | |
| | | 65 | | | | 70 | | | | 75 | | | | | 80 | |
| ttc | aac | aac | ttg | cga | ttg | aag | aat | cca | gaa | tta | acc | acc | atg | att | tca | 288 |
| Phe | Asn | Asn | Leu | Arg | Leu | Lys | Asn | Pro | Glu | Leu | Thr | Thr | Met | Ile | Ser | |
| | | | | 85 | | | | 90 | | | | | | 95 | | |
| ctt | ggt | ggt | tgg | tat | gaa | ggc | tcg | gaa | aaa | tat | tcc | gat | atg | gct | gca | 336 |
| Leu | Gly | Gly | Trp | Tyr | Glu | Gly | Ser | Glu | Lys | Tyr | Ser | Asp | Met | Ala | Ala | |
| | | | 100 | | | | 105 | | | | | 110 | | | | |
| aat | cca | aca | tat | cgt | caa | caa | ttc | ata | caa | tca | ggt | ttg | gac | ttt | ttg | 384 |
| Asn | Pro | Thr | Tyr | Arg | Gln | Gln | Phe | Ile | Gln | Ser | Val | Leu | Asp | Phe | Leu | |
| | | | 115 | | | | 120 | | | | | 125 | | | | |
| caa | gaa | tac | aag | ttc | gac | ggt | cta | gat | ttg | gat | tgg | gag | tat | cct | gga | 432 |
| Gln | Glu | Tyr | Lys | Phe | Asp | Gly | Leu | Asp | Leu | Asp | Trp | Glu | Tyr | Pro | Gly | |
| | | 130 | | | | 135 | | | | | 140 | | | | | |
| tct | cga | ttg | ggt | aac | ccg | aaa | atc | gat | aaa | caa | aac | tat | ttg | gct | ttg | 480 |
| Ser | Arg | Leu | Gly | Asn | Pro | Lys | Ile | Asp | Lys | Gln | Asn | Tyr | Leu | Ala | Leu | |
| | | 145 | | | | 150 | | | | 155 | | | | | 160 | |
| ggt | aga | gaa | ctt | aaa | gac | gct | ttt | gaa | cct | cat | ggc | tac | ttg | ttg | act | 528 |
| Val | Arg | Glu | Leu | Lys | Asp | Ala | Phe | Glu | Pro | His | Gly | Tyr | Leu | Leu | Thr | |
| | | | 165 | | | | | 170 | | | | | 175 | | | |
| gct | gca | gta | tca | cca | ggt | aaa | gac | aaa | atc | gac | cga | gct | tat | gat | atc | 576 |
| Ala | Ala | Val | Ser | Pro | Gly | Lys | Asp | Lys | Ile | Asp | Arg | Ala | Tyr | Asp | Ile | |
| | | | 180 | | | | 185 | | | | | 190 | | | | |
| aaa | gaa | ttg | aac | aaa | ttg | ttc | gat | tgg | atg | aat | gtc | atg | aca | tat | gat | 624 |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Lys | Glu | Leu | Asn | Lys | Leu | Phe | Asp | Trp | Met | Asn | Val | Met | Thr | Tyr | Asp | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| tac | cac | ggt | gga | tgg | gaa | aac | ttt | tac | ggt | cac | aat | gct | ccg | ttg | tat | 672 |
| Tyr | His | Gly | Gly | Trp | Glu | Asn | Phe | Tyr | Gly | His | Asn | Ala | Pro | Leu | Tyr | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| aaa | cga | cca | gat | gaa | act | gat | gag | ttg | cac | act | tac | ttc | aat | gtc | aac | 720 |
| Lys | Arg | Pro | Asp | Glu | Thr | Asp | Glu | Leu | His | Thr | Tyr | Phe | Asn | Val | Asn | |
| | 225 | | | | 230 | | | | | 235 | | | | 240 | | |
| tac | acc | atg | cac | tat | tat | ttg | aac | aat | ggt | gcc | acc | aga | gac | aaa | ttg | 768 |
| Tyr | Thr | Met | His | Tyr | Tyr | Leu | Asn | Asn | Gly | Ala | Thr | Arg | Asp | Lys | Leu | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| gta | atg | ggt | gtt | cca | ttc | tat | ggc | cgt | gct | tgg | agc | att | gaa | gat | cga | 816 |
| Val | Met | Gly | Val | Pro | Phe | Tyr | Gly | Arg | Ala | Trp | Ser | Ile | Glu | Asp | Arg | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| agc | aaa | ctc | aaa | ctt | gga | gat | cca | gcc | aaa | ggc | atg | tcg | ccc | cca | ggt | 864 |
| Ser | Lys | Leu | Lys | Leu | Gly | Asp | Pro | Ala | Lys | Gly | Met | Ser | Pro | Pro | Gly | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| ttc | att | tct | ggt | gaa | gaa | ggt | gtc | ctc | tca | tat | ata | gaa | ttg | tgt | caa | 912 |
| Phe | Ile | Ser | Gly | Glu | Glu | Gly | Val | Leu | Ser | Tyr | Ile | Glu | Leu | Cys | Gln | |
| | 290 | | | | | 295 | | | | | 300 | | | | | |
| ttg | ttt | caa | aaa | gaa | gaa | tgg | cat | atc | caa | tac | gat | gaa | tat | tac | aat | 960 |
| Leu | Phe | Gln | Lys | Glu | Glu | Trp | His | Ile | Gln | Tyr | Asp | Glu | Tyr | Tyr | Asn | |
| | 305 | | | | 310 | | | | | 315 | | | | | 320 | |
| gct | cca | tat | ggt | tac | aat | gat | aaa | atc | tgg | gtc | ggt | tac | gat | gat | ctg | 1008 |
| Ala | Pro | Tyr | Gly | Tyr | Asn | Asp | Lys | Ile | Trp | Val | Gly | Tyr | Asp | Asp | Leu | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| gcc | agt | ata | tca | tgc | aag | ttg | gct | ttc | ctg | aaa | gaa | tta | ggc | gtt | tct | 1056 |
| Ala | Ser | Ile | Ser | Cys | Lys | Leu | Ala | Phe | Leu | Lys | Glu | Leu | Gly | Val | Ser | |
| | | | 340 | | | | | 345 | | | | | 350 | | | |
| ggt | gtc | atg | gtt | tgg | tca | ttg | gaa | aat | gat | gat | ttc | aaa | ggt | cac | tgc | 1104 |
| Gly | Val | Met | Val | Trp | Ser | Leu | Glu | Asn | Asp | Asp | Phe | Lys | Gly | His | Cys | |
| | | 355 | | | | 360 | | | | | 365 | | | | | |
| gga | ccg | aaa | aat | cca | ttg | ttg | aac | aaa | gtt | cat | aat | atg | att | aat | ggc | 1152 |
| Gly | Pro | Lys | Asn | Pro | Leu | Leu | Asn | Lys | Val | His | Asn | Met | Ile | Asn | Gly | |
| | | 370 | | | | 375 | | | | | 380 | | | | | |
| gat | gaa | aag | aac | tct | ttc | gaa | tgc | att | ttg | ggt | cca | agt | aca | acg | aca | 1200 |

Ser Lys Leu Lys Leu Gly Asp Pro Ala Lys Gly Met Ser Pro Pro Gly
 275 280 285

Phe Ile Ser Gly Glu Glu Gly Val Leu Ser Tyr Ile Glu Leu Cys Gln
 290 295 300

Leu Phe Gln Lys Glu Glu Trp His Ile Gln Tyr Asp Glu Tyr Tyr Asn
 305 310 315 320

Ala Pro Tyr Gly Tyr Asn Asp Lys Ile Trp Val Gly Tyr Asp Asp Leu
 325 330 335

Ala Ser Ile Ser Cys Lys Leu Ala Phe Leu Lys Glu Leu Gly Val Ser
 340 345 350

Gly Val Met Val Trp Ser Leu Glu Asn Asp Asp Phe Lys Gly His Cys
 355 360 365

Gly Pro Lys Asn Pro Leu Leu Asn Lys Val His Asn Met Ile Asn Gly
 370 375 380

Asp Glu Lys Asn Ser Phe Glu Cys Ile Leu Gly Pro Ser Thr Thr Thr
 385 390 395 400

Pro Thr Pro Thr Thr Thr Pro Thr Thr Pro Thr Thr Thr Pro Thr Thr
 405 410 415

Pro Ser Pro Thr Thr Pro Thr Thr Thr Pro Ser Pro Thr Thr Pro Thr
 420 425 430

Thr Thr Pro Ser Pro Thr Thr Pro Thr Thr Thr Pro Ser Pro Thr Thr
 435 440 445

Pro Thr Pro Thr Thr Pro Thr Pro Ala Pro Thr Thr Ser Thr Pro Ser
 450 455 460

Pro Thr Thr Thr Glu His Thr Ser Glu Thr Pro Lys Tyr Thr Thr Tyr
 465 470 475 480

Val Asp Gly His Leu Ile Lys Cys Tyr Lys Glu Gly Asp Ile Pro His
 485 490 495

Pro Thr Asn Ile His Lys Tyr Leu Val Cys Glu Phe Val Asn Gly Gly
 500 505 510

Trp Trp Val His Ile Met Pro Cys Pro Pro Gly Thr Ile Trp Cys Gln
 515 520 525

00160-266360

Glu Lys Leu Thr Cys Ile Gly Glu
530 535

<210> 22
<211> 1608
<212> DNA
<213> Dermatophagoides farinae

<400> 22
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atgtgggata tcaccttct tgaacattt gataagatgt ccatcgacat aggttgtata 180
ttttggtgtt tcgcttgtgt gttcgggtcgt ggttggcgaa ggtgtcgatg ttgtaggggc 240
tggtgttggg gttgttgggt ttggtgtggg gggagaagga gttgttgtcg gtgtgggtggg 300
agaagggggt gttgtcgggg ttggtgggaga aggggttgtt gtcgggggtg tgggagaagg 360
agttgttggc gttgtagtgc ggggttgtggg tgtcgtcgtt ggagttggtg tcgttgtact 420
tggacccaaa atgcattcga aagagttctt ttcacgcca ttaatcatat tatgaacttt 480
gttcaacaat ggatttttgc gtcgcgagtg acctttgaaa tcatcatttt ccaatgacca 540
aaccatgaca ccagaaacgc ctaattcttt caggaaagcc aacttgcag atatactggc 600
cagatcatcg taaccgaccc agattttatc attgtaacca tatggagcat tgtaatatc 660
atcgatttgg atatgccatt cttctttttg aaacaattga cacaattcta tatatgagag 720
gacaccttct tcaccagaaa tgaaacctgg gggcgacatg cctttggctg gatctccaag 780
tttgagtttg cttcgatctt caatgctcca agcacggcca tagaatggaa caccattac 840
caatttgtct ctggtggcac cattgttcaa ataatagtgc atggtgtagt tgacattgaa 900
gtaagtgtgc aactcatcag tttcatctgg tcgtttatac aacggagcat tgtgaccgta 960
aaagttttcc catccacgt ggtaatcata tgtcatgaca ttcattcaat cgaacaattt 1020
gttcaattct ttgatatcat aagctcggtc gattttgtct ttacctggtg atactgcagc 1080
agtcaacaag tagccatgag gttcaaaagc gtctttaagt tctctaacca aagccaaata 1140
gttttgttta tcgattttcg ggttacccaa tcgagatcca ggatactccc aatccaaatc 1200
tagaccgtcg aacttgtatt cttgcaaaaa gtccaaaact gattgtatga attgttgacg 1260
atatgttggg tttgcagcca ttcggaata ttttccgag cttcataacc aaccaccaag 1320
tgaaatcatg gtggttaatt ctggattctt caatcgcaag ttgttgaaac gttcataacc 1380
acgtttttcc catgagttat gggtatcatc ttggttaagga tcgaaaactt gaattgtgta 1440
tttgtattca tcaatttttag cgaaaccata cattaaatgt gtacacttga atggatcaat 1500
atcttcgata gtgtatggat caactttatg atatacggac catgttccaa cataacaaac 1560
aattctcatc ggatttttgc aataatcatt atgatctcgt ttgatgga 1608

<210> 23
<211> 25
<212> PRT
<213> Dermatophagoides farinae

<220>
<223> At location 1, Xaa = any amino acid

<400> 23

Xaa Leu Glu Pro Lys Thr Val Cys Tyr Tyr Glu Ser Trp Val His His
1 5 10 15

Arg Gln Gly Glu Gly Lys Met Asp Pro
20 25

<210> 24

<211> 33

<212> PRT

<213> Dermatophagoides farinae

<220>

<223> At locations, 18, 28, 31 and 32, Xaa = any amino
acid

<400> 24

Ser Ile Lys Arg Asp His Asn Asp Tyr Ser Lys Asn Pro Met Met Ile
1 5 10 15

Val Xaa Tyr Gly Gly Ser Ser Gly Tyr Gln Ser Xaa Lys Arg Xaa Xaa
20 25 30

Thr

<210> 25

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<220>

<223> At location 24, n = a, c, t or g

<400> 25

aaacgtgatc ataaygatta ytcnaaraay c

31

<210> 26

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 26

aaacgtgatc ataaygatta yagyaaraay c

31

<210> 27

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<220>

<223> At locations 12 and 21, n = a, c, t or g

<400> 27

ccttcttcac cnacratcaa ncc

23

<210> 28

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<220>

<223> At locations 12 and 21, n = a, c, t or g

<400> 28

ccttcttcac cnacratgaa ncc

23

<210> 29

<211> 13

<212> PRT

<213> Dermatophagoides farinae

<400> 29

Gln Tyr Gly Val Thr Gln Ala Val Val Thr Gln Pro Ala
 1 5 10

<210> 30
 <211> 11
 <212> PRT
 <213> Dermatophagoides farinae

<400> 30
 Asp Glu Leu Leu Met Lys Ser Gly Pro Gly Pro
 1 5 10

<210> 31
 <211> 24
 <212> PRT
 <213> Dermatophagoides farinae

<400> 31
 Asp Met Glu His Phe Thr Gln His Lys Gly Asn Ala Lys Ala Met Ile
 1 5 10 15

Ala Val Gly Gly Ser Thr Met Ser
 20

<210> 32
 <211> 21
 <212> PRT
 <213> Dermatophagoides farinae

<400> 32
 Asp Ala Asn Glu Glu Ala Arg Ser Gln Leu Pro Glu Thr Ala Met Val
 1 5 10 15

Leu Ile Lys Ser Gln
 20

<210> 33
 <211> 21
 <212> PRT
 <213> Dermatophagoides farinae

<400> 33
 Gln Ser Arg Asp Arg Asn Asp Lys Pro Tyr Xaa Ile Val Lys Lys Lys
 1 5 10 15

00460"EB22960

Lys Lys Ala Leu Asp

20

<210> 34

<211> 1621

<212> DNA

<213> Dermatophagoides farinae

<220>

<221> CDS

<222> (14)..(1540)

<400> 34

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Met Lys Thr Thr Phe Ala Leu Phe Cys Ile Trp Ala

1

5

10

tgc att ggc ttg atg aat gcg gcc act aaa cga gat cac aat aat tat 97

Cys Ile Gly Leu Met Asn Ala Ala Thr Lys Arg Asp His Asn Asn Tyr

15

20

25

tcg aaa aat cca atg cga atc gta tgt tat gtt gga aca tgg tcc gtt 145

Ser Lys Asn Pro Met Arg Ile Val Cys Tyr Val Gly Thr Trp Ser Val

30

35

40

tat cat aaa gtt gat cca tac aca att gaa gat att gat cct ttc aaa 193

Tyr His Lys Val Asp Pro Tyr Thr Ile Glu Asp Ile Asp Pro Phe Lys

45

50

55

60

tgt act cat ttg atg tat ggt ttt gct aaa atc gat gaa tac aaa tac 241

Cys Thr His Leu Met Tyr Gly Phe Ala Lys Ile Asp Glu Tyr Lys Tyr

65

70

75

acc att caa gtt ttt gat cca ttt caa gat gat aac cat aac tca tgg 289

Thr Ile Gln Val Phe Asp Pro Phe Gln Asp Asp Asn His Asn Ser Trp

80

85

90

gaa aaa cac ggg tat gaa cgt ttc aac aac ttg aga ttg aag aat cca 337

Glu Lys His Gly Tyr Glu Arg Phe Asn Asn Leu Arg Leu Lys Asn Pro

95

100

105

gaa ttg acc acc atg att tca ttg ggt ggt tgg tat gaa ggt tca gaa 385

Glu Leu Thr Thr Met Ile Ser Leu Gly Gly Trp Tyr Glu Gly Ser Glu

110

115

120

aaa tat tcg gat atg gca gcc aat cca aca tat cgt cag caa ttt gtt 433

| | |
|---|------|
| Lys Tyr Ser Asp Met Ala Ala Asn Pro Thr Tyr Arg Gln Gln Phe Val | |
| 125 130 135 140 | |
| caa tca gtt ttg gac ttt ttg caa gaa tac aaa ttc gat ggc cta gat | 481 |
| Gln Ser Val Leu Asp Phe Leu Gln Glu Tyr Lys Phe Asp Gly Leu Asp | |
| 145 150 155 | |
| ttg gat tgg gaa tat cct gga tca cgg tta ggc aat cct aaa atc gat | 529 |
| Leu Asp Trp Glu Tyr Pro Gly Ser Arg Leu Gly Asn Pro Lys Ile Asp | |
| 160 165 170 | |
| aaa caa aac tat tta aca tta gtt aga gaa ctt aaa gag gca ttt gaa | 577 |
| Lys Gln Asn Tyr Leu Thr Leu Val Arg Glu Leu Lys Glu Ala Phe Glu | |
| 175 180 185 | |
| cct ttc ggc tac ttg ttg act gcc gca gta tca ccc ggt aaa gat aaa | 625 |
| Pro Phe Gly Tyr Leu Leu Thr Ala Ala Val Ser Pro Gly Lys Asp Lys | |
| 190 195 200 | |
| att gac gta gct tat gag ctc aaa gaa ttg aac caa ttg ttc gat tgg | 673 |
| Ile Asp Val Ala Tyr Glu Leu Lys Glu Leu Asn Gln Leu Phe Asp Trp | |
| 205 210 215 220 | |
| atg aat gtc atg act tat gat tac cat ggc gga tgg gaa aat gtt ttc | 721 |
| Met Asn Val Met Thr Tyr Asp Tyr His Gly Gly Trp Glu Asn Val Phe | |
| 225 230 235 | |
| ggc cat aat gct ccg ttg tat aaa cga ccc gat gaa acg gat gaa ttg | 769 |
| Gly His Asn Ala Pro Leu Tyr Lys Arg Pro Asp Glu Thr Asp Glu Leu | |
| 240 245 250 | |
| cac act tac ttc aat gtc aac tac acc atg cac tat tat ttg aac aat | 817 |
| His Thr Tyr Phe Asn Val Asn Tyr Thr Met His Tyr Tyr Leu Asn Asn | |
| 255 260 265 | |
| ggc gct act cga gac aaa ctt gtt atg ggt gtt cca ttc tat ggt cgt | 865 |
| Gly Ala Thr Arg Asp Lys Leu Val Met Gly Val Pro Phe Tyr Gly Arg | |
| 270 275 280 | |
| gct tgg agc atc gaa gat cga agc aaa gtc aaa ctt ggc gat ccg gcc | 913 |
| Ala Trp Ser Ile Glu Asp Arg Ser Lys Val Lys Leu Gly Asp Pro Ala | |
| 285 290 295 300 | |
| aaa ggc atg tct cct cct ggt ttt att act ggt gaa gaa ggt gtt ctc | 961 |
| Lys Gly Met Ser Pro Pro Gly Phe Ile Thr Gly Glu Glu Gly Val Leu | |
| 305 310 315 | |
| tca tac atc gaa ttg tgt cag tta ttc cag aaa gaa gaa tgg cat att | 1009 |

| | |
|---|------|
| Ser Tyr Ile Glu Leu Cys Gln Leu Phe Gln Lys Glu Glu Trp His Ile | |
| 320 325 330 | |
| caa tac gat gaa tat tac aat gct cca tac gga tat aat gat aaa atc | 1057 |
| Gln Tyr Asp Glu Tyr Tyr Asn Ala Pro Tyr Gly Tyr Asn Asp Lys Ile | |
| 335 340 345 | |
| tgg gtt ggt tac gat gat ctg gct agt ata tca tgc aag ttg gcc ttt | 1105 |
| Trp Val Gly Tyr Asp Asp Leu Ala Ser Ile Ser Cys Lys Leu Ala Phe | |
| 350 355 360 | |
| ctc aaa gaa ttg ggc gtc tct ggc gtt atg ata tgg tca ttg gaa aac | 1153 |
| Leu Lys Glu Leu Gly Val Ser Gly Val Met Ile Trp Ser Leu Glu Asn | |
| 365 370 375 380 | |
| gat gat ttc aaa ggt cat tgc gga ccg aaa tat cca ttg ttg aac aaa | 1201 |
| Asp Asp Phe Lys Gly His Cys Gly Pro Lys Tyr Pro Leu Leu Asn Lys | |
| 385 390 395 | |
| gtt cac aat atg atc aat ggt gat gaa aag aac tct tac gaa tgt ctt | 1249 |
| Val His Asn Met Ile Asn Gly Asp Glu Lys Asn Ser Tyr Glu Cys Leu | |
| 400 405 410 | |
| ttg ggc cca agt aca acc aca cca aca cca acc acc ccg tca act act | 1297 |
| Leu Gly Pro Ser Thr Thr Thr Pro Thr Pro Thr Thr Pro Ser Thr Thr | |
| 415 420 425 | |
| tcg act acc aca cca acg cct acc acc acc gat agc aca agc gaa aca | 1345 |
| Ser Thr Thr Thr Pro Thr Pro Thr Thr Thr Asp Ser Thr Ser Glu Thr | |
| 430 435 440 | |
| cca aaa tac act acg tat att gat gga cat ttg att aaa tgc tat aaa | 1393 |
| Pro Lys Tyr Thr Thr Tyr Ile Asp Gly His Leu Ile Lys Cys Tyr Lys | |
| 445 450 455 460 | |
| caa ggt tat ctt cca cat cca act gat gtt cat aaa tat tta gtt tgt | 1441 |
| Gln Gly Tyr Leu Pro His Pro Thr Asp Val His Lys Tyr Leu Val Cys | |
| 465 470 475 | |
| gaa tat att gcc aca cca aac ggt ggt tgg tgg gta cac att atg gat | 1489 |
| Glu Tyr Ile Ala Thr Pro Asn Gly Gly Trp Trp Val His Ile Met Asp | |
| 480 485 490 | |
| tgt cca aaa gga act aga tgg cac gca aca tta aaa aat tgt att caa | 1537 |
| Cys Pro Lys Gly Thr Arg Trp His Ala Thr Leu Lys Asn Cys Ile Gln | |
| 495 500 505 | |
| gaa tgatctgata tatttgtaac tgttttttgc taaatgaaat ttaaataaaa | 1590 |

[illegible]

1621

<211> 509

<213> Dermatophagoides farinae

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Thr | Thr | Phe | Ala | Leu | Phe | Cys | Ile | Trp | Ala | Cys | Ile | Gly | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

Met Asn Ala Ala Thr Lys Arg Asp His Asn Asn Tyr Ser Lys Asn Pro
20 25 30

Met Arg Ile Val Cys Tyr Val Gly Thr Trp Ser Val Tyr His Lys Val
35 40 45

Asp Pro Tyr Thr Ile Glu Asp Ile Asp Pro Phe Lys Cys Thr His Leu
50 55 60

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Tyr | Gly | Phe | Ala | Lys | Ile | Asp | Glu | Tyr | Lys | Tyr | Thr | Ile | Gln | Val |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |

Phe. Asp Pro Phe Gln Asp Asp Asn His Asn Ser Trp Glu Lys His Gly
85 90 95

Tyr Glu Arg Phe Asn Asn Leu Arg Leu Lys Asn Pro Glu Leu Thr Thr
100 105 110

Met Ile Ser Leu Gly Gly Trp Tyr Glu Gly Ser Glu Lys Tyr Ser Asp
115 120 125

Met Ala Ala Asn Pro Thr Tyr Arg Gln Gln Phe Val Gln Ser Val Leu
130 135 140

Asp Phe Leu Gln Glu Tyr Lys Phe Asp Gly Leu Asp Leu Asp Trp Glu
145 150 155 160

Tyr Pro Gly Ser Arg Leu Gly Asn Pro Lys Ile Asp Lys Gln Asn Tyr
165 170 175

Leu Thr Leu Val Arg Glu Leu Lys Glu Ala Phe Glu Pro Phe Gly Tyr
180 185 190

30

195

200

205

Tyr Glu Leu Lys Glu Leu Asn Gln Leu Phe Asp Trp Met Asn Val Met
210 215 220

Thr Tyr Asp Tyr His Gly Gly Trp Glu Asn Val Phe Gly His Asn Ala
225 230 235 240

Pro Leu Tyr Lys Arg Pro Asp Glu Thr Asp Glu Leu His Thr Tyr Phe
245 250 255

Asn Val Asn Tyr Thr Met His Tyr Tyr Leu Asn Asn Gly Ala Thr Arg
260 265 270

Asp Lys Leu Val Met Gly Val Pro Phe Tyr Gly Arg Ala Trp Ser Ile
275 280 285

Glu Asp Arg Ser Lys Val Lys Leu Gly Asp Pro Ala Lys Gly Met Ser
290 295 300

Pro Pro Gly Phe Ile Thr Gly Glu Glu Gly Val Leu Ser Tyr Ile Glu
305 310 315 320

Leu Cys Gln Leu Phe Gln Lys Glu Glu Trp His Ile Gln Tyr Asp Glu
325 330 335

Tyr Tyr Asn Ala Pro Tyr Gly Tyr Asn Asp Lys Ile Trp Val Gly Tyr
340 345 350

Asp Asp Leu Ala Ser Ile Ser Cys Lys Leu Ala Phe Leu Lys Glu Leu
355 360 365

Gly Val Ser Gly Val Met Ile Trp Ser Leu Glu Asn Asp Asp Phe Lys
370 375 380

Gly His Cys Gly Pro Lys Tyr Pro Leu Leu Asn Lys Val His Asn Met
385 390 395 400

Ile Asn Gly Asp Glu Lys Asn Ser Tyr Glu Cys Leu Leu Gly Pro Ser
405 410 415

Thr Thr Thr Pro Thr Pro Thr Thr Pro Ser Thr Thr Ser Thr Thr Thr
420 425 430

Pro Thr Pro Thr Thr Thr Asp Ser Thr Ser Glu Thr Pro Lys Tyr Thr
435 440 445

Thr Tyr Ile Asp Gly His Leu Ile Lys Cys Tyr Lys Gln Gly Tyr Leu

001160-262990

450

455

460

Pro His Pro Thr Asp Val His Lys Tyr Leu Val Cys Glu Tyr Ile Ala
 465 470 475 480

Thr Pro Asn Gly Gly Trp Trp Val His Ile Met Asp Cys Pro Lys Gly
 485 490 495

Thr Arg Trp His Ala Thr Leu Lys Asn Cys Ile Gln Glu
 500 505

<210> 36

<211> 1621

<212> DNA

<213> Dermatophagoides farinae

<400> 36

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 tccttttgga caatccataa tgtgtacca ccaaccaccg tttggtgtgg caatatattc 180
 acaaactaaa tatttatgaa catcagttgg atgtggaaga taacctgtt tatagcattt 240
 aatcaaagt ccatcaatat acgtagtgt ttttgggtgt tcgcttgtgc tatcggtggt 300
 ggtaggcggt ggtgtggtag tcgaagtagt tgacgggggtg gttggtgttg gtgtggttgt 360
 acttggggccc aaaagacatt cgtaagagtt cttttcatca ccattgatca tattgtgaac 420
 tttgttcaac aatggatatt tcgggtccgca atgaccttg aaatcatcgt tttccaatga 480
 ccatatcata acgccagaga cgcccaattc tttgagaaag gccaaacttg atgatatact 540
 agccagatca tcgtaaccaa cccagatttt atcattatat ccgtatggag cattgtaata 600
 ttcacgtgat tgaatatgcc attcttcttt ctggaataac tgacacaatt cgatgtatga 660
 gagaacacct tcttcaccag taataaaacc aggaggagac atgcctttgg ccggatcgcc 720
 aagtttgact ttgcttcgat cttcgatgct ccaagcacga ccatagaatg gaacacccat 780
 aacaagtttg tctcgagtag cgccattgtt caaataatag tgcattggtg agttgacatt 840
 gaagtaagt tgcaattcat cgttttcac gggtcgttta tacaacggag cattatggcc 900
 gaaaacattt tcccatccgc catggtaatc ataagtcag acattcatcc aatcgaacaa 960
 ttggttcaat tctttgagct cataagctac gtcaatttta tctttaccgg gtgatactgc 1020
 ggcagtcaac aagtagccga aagggttcaa tgctcttta agttctctaa ctaatgttaa 1080
 atagttttgt ttatcgattt taggattgcc taaccgtgat ccaggatatt cccaatccaa 1140
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 acgatatgtt ggattggctg ccatatccga atatttttct gaaccttcat accaaccacc 1260
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 gtatttgtat tcatcgattt tagcaaaacc atacatcaaa tgagtacatt tgaaaggatc 1440
 aatatcttca attgtgtatg gatcaacttt atgataaacg gaccatgttc caacataaca 1500
 tacgattcgc attggatttt tcgaataatt attgtgatct cgttttagtgg ccgcattcat 1560
 caagccaatg caggcccata tacaaaacaa tgcaaatgtc gttttcattt tcataagttc 1620
 t 1621

Table 1

Table 1

Table 1

| | |
|---|------|
| Asp Phe Leu Gln Glu Tyr Lys Phe Asp Gly Leu Asp Leu Asp Trp Glu | |
| 145 150 155 160 | |
| tat cct gga tca cgg tta ggc aat cct aaa atc gat aaa caa aac tat | 528 |
| Tyr Pro Gly Ser Arg Leu Gly Asn Pro Lys Ile Asp Lys Gln Asn Tyr | |
| 165 170 175 | |
| tta aca tta gtt aga gaa ctt aaa gag gca ttt gaa cct ttc ggc tac | 576 |
| Leu Thr Leu Val Arg Glu Leu Lys Glu Ala Phe Glu Pro Phe Gly Tyr | |
| 180 185 190 | |
| ttg ttg act gcc gca gta tca ccc ggt aaa gat aaa att gac gta gct | 624 |
| Leu Leu Thr Ala Ala Val Ser Pro Gly Lys Asp Lys Ile Asp Val Ala | |
| 195 200 205 | |
| tat gag ctc aaa gaa ttg aac caa ttg ttc gat tgg atg aat gtc atg | 672 |
| Tyr Glu Leu Lys Glu Leu Asn Gln Leu Phe Asp Trp Met Asn Val Met | |
| 210 215 220 | |
| act tat gat tac cat ggc gga tgg gaa aat gtt ttc ggc cat aat gct | 720 |
| Thr Tyr Asp Tyr His Gly Gly Trp Glu Asn Val Phe Gly His Asn Ala | |
| 225 230 235 240 | |
| ccg ttg tat aaa cga ccc gat gaa acg gat gaa ttg cac act tac ttc | 768 |
| Pro Leu Tyr Lys Arg Pro Asp Glu Thr Asp Glu Leu His Thr Tyr Phe | |
| 245 250 255 | |
| aat gtc aac tac acc atg cac tat tat ttg aac aat ggc gct act cga | 816 |
| Asn Val Asn Tyr Thr Met His Tyr Tyr Leu Asn Asn Gly Ala Thr Arg | |
| 260 265 270 | |
| gac aaa ctt gtt atg ggt gtt cca ttc tat ggt cgt gct tgg agc atc | 864 |
| Asp Lys Leu Val Met Gly Val Pro Phe Tyr Gly Arg Ala Trp Ser Ile | |
| 275 280 285 | |
| gaa gat cga agc aaa gtc aaa ctt ggc gat ccg gcc aaa ggc atg tct | 912 |
| Glu Asp Arg Ser Lys Val Lys Leu Gly Asp Pro Ala Lys Gly Met Ser | |
| 290 295 300 | |
| cct cct ggt ttt att act ggt gaa gaa ggt gtt ctc tca tac atc gaa | 960 |
| Pro Pro Gly Phe Ile Thr Gly Glu Glu Gly Val Leu Ser Tyr Ile Glu | |
| 305 310 315 320 | |
| ttg tgt cag tta ttc cag aaa gaa gaa tgg cat att caa tac gat gaa | 1008 |
| Leu Cys Gln Leu Phe Gln Lys Glu Glu Trp His Ile Gln Tyr Asp Glu | |
| 325 330 335 | |
| tat tac aat gct cca tac gga tat aat gat aaa atc tgg gtt ggt tac | 1056 |

| | |
|---|------|
| Tyr Tyr Asn Ala Pro Tyr Gly Tyr Asn Asp Lys Ile Trp Val Gly Tyr | |
| 340 345 350 | |
| gat gat ctg gct agt ata tca tgc aag ttg gcc ttt ctc aaa gaa ttg | 1104 |
| Asp Asp Leu Ala Ser Ile Ser Cys Lys Leu Ala Phe Leu Lys Glu Leu | |
| 355 360 365 | |
| ggc gtc tct ggc gtt atg ata tgg tca ttg gaa aac gat gat ttc aaa | 1152 |
| Gly Val Ser Gly Val Met Ile Trp Ser Leu Glu Asn Asp Asp Phe Lys | |
| 370 375 380 | |
| ggc cat tgc gga ccg aaa tat cca ttg ttg aac aaa gtt cac aat atg | 1200 |
| Gly His Cys Gly Pro Lys Tyr Pro Leu Leu Asn Lys Val His Asn Met | |
| 385 390 395 400 | |
| atc aat ggt gat gaa aag aac tct tac gaa tgt ctt ttg ggc cca agt | 1248 |
| Ile Asn Gly Asp Glu Lys Asn Ser Tyr Glu Cys Leu Leu Gly Pro Ser | |
| 405 410 415 | |
| aca acc aca cca aca cca acc acc ccg tca act act tcg act acc aca | 1296 |
| Thr Thr Thr Pro Thr Pro Thr Thr Pro Ser Thr Thr Ser Thr Thr Thr | |
| 420 425 430 | |
| cca acg cct acc acc acc gat agc aca agc gaa aca cca aaa tac act | 1344 |
| Pro Thr Pro Thr Thr Thr Asp Ser Thr Ser Glu Thr Pro Lys Tyr Thr | |
| 435 440 445 | |
| acg tat att gat gga cat ttg att aaa tgc tat aaa caa ggt tat ctt | 1392 |
| Thr Tyr Ile Asp Gly His Leu Ile Lys Cys Tyr Lys Gln Gly Tyr Leu | |
| 450 455 460 | |
| cca cat cca act gat gtt cat aaa tat tta gtt tgt gaa tat att gcc | 1440 |
| Pro His Pro Thr Asp Val His Lys Tyr Leu Val Cys Glu Tyr Ile Ala | |
| 465 470 475 480 | |
| aca cca aac ggt ggt tgg tgg gta cac att atg gat tgt cca aaa gga | 1488 |
| Thr Pro Asn Gly Gly Trp Trp Val His Ile Met Asp Cys Pro Lys Gly | |
| 485 490 495 | |
| act aga tgg cac gca aca tta aaa aat tgt att caa gaa | 1527 |
| Thr Arg Trp His Ala Thr Leu Lys Asn Cys Ile Gln Glu | |
| 500 505 | |

<210> 38
 <211> 509
 <212> PRT
 <213> Dermatophagoides farinae

<400> 38

Met Lys Thr Thr Phe Ala Leu Phe Cys Ile Trp Ala Cys Ile Gly Leu
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Met Asn Ala Ala Thr Lys Arg Asp His Asn Asn Tyr Ser Lys Asn Pro
20 25 30

Met Arg Ile Val Cys Tyr Val Gly Thr Trp Ser Val Tyr His Lys Val
35 40 45

Asp Pro Tyr Thr Ile Glu Asp Ile Asp Pro Phe Lys Cys Thr His Leu
50 55 60

Met Tyr Gly Phe Ala Lys Ile Asp Glu Tyr Lys Tyr Thr Ile Gln Val
65 70 75 80

Phe Asp Pro Phe Gln Asp Asp Asn His Asn Ser Trp Glu Lys His Gly
85 90 95

Tyr Glu Arg Phe Asn Asn Leu Arg Leu Lys Asn Pro Glu Leu Thr Thr
100 105 110

Met Ile Ser Leu Gly Gly Trp Tyr Glu Gly Ser Glu Lys Tyr Ser Asp
115 120 125

Met Ala Ala Asn Pro Thr Tyr Arg Gln Gln Phe Val Gln Ser Val Leu
130 135 140

Asp Phe Leu Gln Glu Tyr Lys Phe Asp Gly Leu Asp Leu Asp Trp Glu
145 150 155 160

Tyr Pro Gly Ser Arg Leu Gly Asn Pro Lys Ile Asp Lys Gln Asn Tyr
165 170 175

Leu Thr Leu Val Arg Glu Leu Lys Glu Ala Phe Glu Pro Phe Gly Tyr
180 185 190

Leu Leu Thr Ala Ala Val Ser Pro Gly Lys Asp Lys Ile Asp Val Ala
195 200 205

Tyr Glu Leu Lys Glu Leu Asn Gln Leu Phe Asp Trp Met Asn Val Met
210 215 220

Thr Tyr Asp Tyr His Gly Gly Trp Glu Asn Val Phe Gly His Asn Ala
225 230 235 240

Pro Leu Tyr Lys Arg Pro Asp Glu Thr Asp Glu Leu His Thr Tyr Phe

00160-6629900

245

250

255

Asn Val Asn Tyr Thr Met His Tyr Tyr Leu Asn Asn Gly Ala Thr Arg
260 265 270

Asp Lys Leu Val Met Gly Val Pro Phe Tyr Gly Arg Ala Trp Ser Ile
275 280 285

Glu Asp Arg Ser Lys Val Lys Leu Gly Asp Pro Ala Lys Gly Met Ser
290 295 300

Pro Pro Gly Phe Ile Thr Gly Glu Glu Gly Val Leu Ser Tyr Ile Glu
305 310 315 320

Leu Cys Gln Leu Phe Gln Lys Glu Glu Trp His Ile Gln Tyr Asp Glu
325 330 335

Tyr Tyr Asn Ala Pro Tyr Gly Tyr Asn Asp Lys Ile Trp Val Gly Tyr
340 345 350

Asp Asp Leu Ala Ser Ile Ser Cys Lys Leu Ala Phe Leu Lys Glu Leu
355 360 365

Gly Val Ser Gly Val Met Ile Trp Ser Leu Glu Asn Asp Asp Phe Lys
370 375 380

Gly His Cys Gly Pro Lys Tyr Pro Leu Leu Asn Lys Val His Asn Met
385 390 395 400

Ile Asn Gly Asp Glu Lys Asn Ser Tyr Glu Cys Leu Leu Gly Pro Ser
405 410 415

Thr Thr Thr Pro Thr Pro Thr Thr Pro Ser Thr Thr Ser Thr Thr Thr
420 425 430

Pro Thr Pro Thr Thr Thr Asp Ser Thr Ser Glu Thr Pro Lys Tyr Thr
435 440 445

Thr Tyr Ile Asp Gly His Leu Ile Lys Cys Tyr Lys Gln Gly Tyr Leu
450 455 460

Pro His Pro Thr Asp Val His Lys Tyr Leu Val Cys Glu Tyr Ile Ala
465 470 475 480

Thr Pro Asn Gly Gly Trp Trp Val His Ile Met Asp Cys Pro Lys Gly
485 490 495

Thr Arg Trp His Ala Thr Leu Lys Asn Cys Ile Gln Glu

<210> 39
 <211> 1527
 <212> DNA
 <213> *Dermatophagoides farinae*

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 atcagttgga tgtggaagat aaccttgttt atagcattta atcaaatgtc catcaatata 180
 cgtagtgtat tttggtgttt cgcttgTgct atcggTggTg gtaggcgttg gtgtggtagt 240
 cgaagtagtt gacggggTgg ttggtgtTgg tgtggtTgta cttgggcca aaagacattc 300
 gtaagagttc ttttcatcac cattgatcat attgtgaact ttgttcaaca atggatattt 360
 cggTccgcaa tgacctttga aatcatcgTt ttccaatgac catatcataa cgccagagac 420
 gcccaattct ttgagaaagg ccaacttgca tgatatacta gccagatcat cgtaaccaac 480
 ccagatttta tcattatata cgtatggagc attgtaatat tcatcgTatt gaatatgcca 540
 ttcttctttc tggaaataact gacacaattc gatgtatgag agaacacctt cttcaccagt 600
 aataaaacca ggaggagaca tgcctttggc cggatcgcca agtttgactt tgcttcgatac 660
 ttcgatgctc caagcacgac catagaatgg aacaccata acaagtttgt ctcgagtagc 720
 gccattgttc aaataatagt gcatggtgta gttgacattg aagtaagtgt gcaattcatc 780
 cgtttcatcg ggtcgTttat acaacggagc attatggccg aaaacatttt cccatccgcc 840
 atggtaatca taagtcataga cattcatcca atcgaacaat tggTtcaatt ctttgagctc 900
 ataagctacg tcaattttat ctttaccggg tgatactgcg gcagtcaaca agtagccgaa 960
 aggttcaa at gcctctttta gttctctaac taatgttaaa tagttttgtt tatcgatttt 1020
 aggattgcct aaccgtgate caggatatc ccaatccaaa tctaggccat cgaatttgta 1080
 ttcttgcaaa aagtccaaaa ctgattgaac aaattgctga cgatatgttg gattggctgc 1140
 catatccgaa tattttttctg aaccttcata ccaaccacc aatgaaatca tggTggTcaa 1200
 ttctggattc ttcaatctca agttgttgaa acgttcatac ccgtgttttt cccatgagtt 1260
 atggTtatca tcttgaaatg gatcaaaaaac ttgaatggTg tatttgTatt catcgatttt 1320
 agcaaaacca tacatcaaat gagtacattt gaaaggatca atatcttcaa ttgtgtatgg 1380
 atcaacttta tgataaacgg accatgttcc aacataacat acgattcgca ttggattttt 1440
 cgaataatta ttgtgatctc gtttagtggc cgcattcatc aagccaatgc aggccatat 1500
 acaaaacaat gcaaatgtcg ttttcat 1527

<210> 40
 <211> 1470
 <212> DNA
 <213> *Dermatophagoides farinae*

<220>
 <221> CDS
 <222> (1)..(1470)

<400> 40

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| Lys Glu Leu Asn Gln Leu Phe Asp Trp Met Asn Val Met Thr Tyr Asp | |
| 195 200 205 | |
| tac cat ggc gga tgg gaa aat gtt ttc ggc cat aat gct ccg ttg tat | 672 |
| Tyr His Gly Gly Trp Glu Asn Val Phe Gly His Asn Ala Pro Leu Tyr | |
| 210 215 220 | |
| aaa cga ccc gat gaa acg gat gaa ttg cac act tac ttc aat gtc aac | 720 |
| Lys Arg Pro Asp Glu Thr Asp Glu Leu His Thr Tyr Phe Asn Val Asn | |
| 225 230 235 240 | |
| tac acc atg cac tat tat ttg aac aat ggc gct act cga gac aaa ctt | 768 |
| Tyr Thr Met His Tyr Tyr Leu Asn Asn Gly Ala Thr Arg Asp Lys Leu | |
| 245 250 255 | |
| gtt atg ggt gtt cca ttc tat ggt cgt gct tgg agc atc gaa gat cga | 816 |
| Val Met Gly Val Pro Phe Tyr Gly Arg Ala Trp Ser Ile Glu Asp Arg | |
| 260 265 270 | |
| agc aaa gtc aaa ctt ggc gat ccg gcc aaa ggc atg tct cct cct ggt | 864 |
| Ser Lys Val Lys Leu Gly Asp Pro Ala Lys Gly Met Ser Pro Pro Gly | |
| 275 280 285 | |
| ttt att act ggt gaa gaa ggt gtt ctc tca tac atc gaa ttg tgt cag | 912 |
| Phe Ile Thr Gly Glu Glu Gly Val Leu Ser Tyr Ile Glu Leu Cys Gln | |
| 290 295 300 | |
| tta ttc cag aaa gaa gaa tgg cat att caa tac gat gaa tat tac aat | 960 |
| Leu Phe Gln Lys Glu Glu Trp His Ile Gln Tyr Asp Glu Tyr Tyr Asn | |
| 305 310 315 320 | |
| gct cca tac gga tat aat gat aaa atc tgg gtt ggt tac gat gat ctg | 1008 |
| Ala Pro Tyr Gly Tyr Asn Asp Lys Ile Trp Val Gly Tyr Asp Asp Leu | |
| 325 330 335 | |
| gct agt ata tca tgc aag ttg gcc ttt ctc aaa gaa ttg ggc gtc tct | 1056 |
| Ala Ser Ile Ser Cys Lys Leu Ala Phe Leu Lys Glu Leu Gly Val Ser | |
| 340 345 350 | |
| ggc gtt atg ata tgg tca ttg gaa aac gat gat ttc aaa ggt cat tgc | 1104 |
| Gly Val Met Ile Trp Ser Leu Glu Asn Asp Asp Phe Lys Gly His Cys | |
| 355 360 365 | |
| gga ccg aaa tat cca ttg ttg aac aaa gtt cac aat atg atc aat ggt | 1152 |
| Gly Pro Lys Tyr Pro Leu Leu Asn Lys Val His Asn Met Ile Asn Gly | |
| 370 375 380 | |

gat gaa aag aac tct tac gaa tgt ctt ttg ggc cca agt aca acc aca 1200
 Asp Glu Lys Asn Ser Tyr Glu Cys Leu Leu Gly Pro Ser Thr Thr Thr
 385 390 395 400

cca aca cca acc acc ccg tca act act tcg act acc aca cca acg cct 1248
 Pro Thr Pro Thr Thr Pro Ser Thr Thr Ser Thr Thr Thr Pro Thr Pro
 405 410 415

acc acc acc gat agc aca agc gaa aca cca aaa tac act acg tat att 1296
 Thr Thr Thr Asp Ser Thr Ser Glu Thr Pro Lys Tyr Thr Thr Tyr Ile
 420 425 430

gat gga cat ttg att aaa tgc tat aaa caa ggt tat ctt cca cat cca 1344
 Asp Gly His Leu Ile Lys Cys Tyr Lys Gln Gly Tyr Leu Pro His Pro
 435 440 445

act gat gtt cat aaa tat tta gtt tgt gaa tat att gcc aca cca aac 1392
 Thr Asp Val His Lys Tyr Leu Val Cys Glu Tyr Ile Ala Thr Pro Asn
 450 455 460

ggg ggt tgg tgg gta cac att atg gat tgt cca aaa gga act aga tgg 1440
 Gly Gly Trp Trp Val His Ile Met Asp Cys Pro Lys Gly Thr Arg Trp
 465 470 475 480

cac gca aca tta aaa aat tgt att caa gaa 1470
 His Ala Thr Leu Lys Asn Cys Ile Gln Glu
 485 490

<210> 41
 <211> 490
 <212> PRT
 <213> Dermatophagoides farinae

<400> 41
 Ala Thr Lys Arg Asp His Asn Asn Tyr Ser Lys Asn Pro Met Arg Ile
 1 5 10 15

Val Cys Tyr Val Gly Thr Trp Ser Val Tyr His Lys Val Asp Pro Tyr
 20 25 30

Thr Ile Glu Asp Ile Asp Pro Phe Lys Cys Thr His Leu Met Tyr Gly
 35 40 45

Phe Ala Lys Ile Asp Glu Tyr Lys Tyr Thr Ile Gln Val Phe Asp Pro
 50 55 60

Phe Gln Asp Asp Asn His Asn Ser Trp Glu Lys His Gly Tyr Glu Arg

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270

285

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320

Ala Pro Tyr Gly Tyr Asn Asp Lys Ile Trp Val Gly Tyr Asp Asp Leu

325

330

335

Ala Ser Ile Ser Cys Lys Leu Ala Phe Leu Lys Glu Leu Gly Val Ser
340 345 350

Gly Val Met Ile Trp Ser Leu Glu Asn Asp Asp Phe Lys Gly His Cys
355 360 365

Gly Pro Lys Tyr Pro Leu Leu Asn Lys Val His Asn Met Ile Asn Gly
370 375 380

Asp Glu Lys Asn Ser Tyr Glu Cys Leu Leu Gly Pro Ser Thr Thr Thr
385 390 395 400

Pro Thr Pro Thr Thr Pro Ser Thr Thr Ser Thr Thr Thr Pro Thr Pro
405 410 415

Thr Thr Thr Asp Ser Thr Ser Glu Thr Pro Lys Tyr Thr Thr Tyr Ile
420 425 430

Asp Gly His Leu Ile Lys Cys Tyr Lys Gln Gly Tyr Leu Pro His Pro
435 440 445

Thr Asp Val His Lys Tyr Leu Val Cys Glu Tyr Ile Ala Thr Pro Asn
450 455 460

Gly Gly Trp Trp Val His Ile Met Asp Cys Pro Lys Gly Thr Arg Trp
465 470 475 480

His Ala Thr Leu Lys Asn Cys Ile Gln Glu
485 490

<210> 42

<211> 1470

<212> DNA

<213> Dermatophagoides farinae

<400> 42

ttcttgaata caatTTTTTA atgttgCGtg ccatctagtt ccttttggac aatccataat 60
gtgtacccac caaccaccgt ttggtgtggc aatatattca caaactaaat atttatgaac 120
atcagttgga tgtggaagat aacctgtgtt atagcattta atcaaagtgc catcaatata 180
cgtagtgtat tttggtgttt cgcttgTgct atcggtggtg gtaggcgttg gtgtggtagt 240
cgaagtagtt gacggggtgg ttggtgttg tgtggttgta cttggggcca aaagacattc 300
gtaagagttc ttttcatcac cattgatcat attgtgaact ttgttcaaca atggatattt 360
cgggtccgcaa tgacctttga aatcatcggt ttccaatgac catatcataa cgccagagac 420
gccaattct ttgagaaagg ccaacttgca tgatatacta gccagatcat cgtaaccaac 480

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ccagatttta tcattatata cgtatggagc attgtaatat tcatcgtatt gaatatgcc 540
ttctttctttc tggaataact gacacaattc gatgtatgag agaacacctt cttcaccagt 600
aataaaacca ggaggagaca tgcctttggc cggatcgcca agtttgactt tgcttcgac 660
ttcgatgctc caagcacgac catagaatgg aacaccata acaagtttgt ctcgagtagc 720
gccattgttc aaataatagt gcatggtgta gttgacattg aagtaagtgt gcaattcatc 780
cgtttcatcg ggtcgtttat acaacggagc attatggccg aaaacatttt cccatccgcc 840
atggtaatca taagtcatga cattcatcca atcgaacaat tggttcaatt ctttgagctc 900
ataagctacg tcaattttat ctttaccggg tgatactgcg gcagtcaaca agtagccgaa 960
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ttcttgcaaa aagtccaaaa ctgattgaac aaattgctga cgatatgttg gattggctgc 1140
catatccgaa tatttttctg aaccttcata ccaaccacc aatgaaatca tgggtggtaa 1200
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agcaaaacca tacatcaaat gagtacattt gaaaggatca atatcttcaa ttgtgtatgg 1380
atcaacttta tgataaacgg accatgttcc aacataacat acgattcgca ttggattttt 1440
cgaataatta ttgtgatctc gtttagtggc 1470

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<210> 43
<211> 510
<212> DNA
<213> Dermatophagoides farinae

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<220>
<221> CDS
<222> (1)..(510)

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<400> 43
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Asp Met Glu His Phe Thr Gln His Lys Gly Asn Ala Lys Ala Met Ile
1 5 10 15

gcc gtc ggt ggt tcg act atg tcc gat caa ttt tcc aag act gca gcg 96
Ala Val Gly Gly Ser Thr Met Ser Asp Gln Phe Ser Lys Thr Ala Ala
20 25 30

gta gaa cat tat cgg gaa acg ttt gtt gtt agc aca gtt gat ctt atg 144
Val Glu His Tyr Arg Glu Thr Phe Val Val Ser Thr Val Asp Leu Met
35 40 45

act cgt tat ggt ttc gat ggt gtc atg att gat tgg tct ggc atg caa 192
Thr Arg Tyr Gly Phe Asp Gly Val Met Ile Asp Trp Ser Gly Met Gln
50 55 60

gcc aaa gat agt gat aat ttc att aaa ttg ttg gac aaa ttc gac gaa 240
Ala Lys Asp Ser Asp Asn Phe Ile Lys Leu Leu Asp Lys Phe Asp Glu
65 70 75 80

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001160-600000

Ile Ala Ser Tyr Asp Asn Tyr Asn Ile Pro Ala Ile Ser Asn Tyr Val
 100 105 110

Asp Phe Met Asn Val Leu Ser Leu Asp Tyr Thr Gly Ser Trp Ala His
 115 120 125

Thr Val Gly His Ala Ser Pro Phe Pro Glu Gln Leu Lys Thr Leu Glu
 130 135 140

Ala Tyr His Lys Arg Gly Ala Pro Arg His Lys Met Val Met Ala Val
 145 150 155 160

Pro Phe Tyr Ala Arg Thr Trp Ile Leu Glu
 165 170

<210> 45

<211> 510

<212> DNA

<213> Dermatophagoides farinae

<400> 45

ctcgagaatc caggtacgtg cataaaatgg tacagccatg accatcttat gacgtggagc 60
 gcctcgtttg tggtaagctt ctagcgtttt gagttgttca ggaaacggag aagcatgacc 120
 gaccgatg gcccatgatac cagtgtgaatc cagactaagc acgttcataa aatcgacata 180
 gttggagatg gcaggaatgt tatagttatc gtatgatgac atcggttgccg gcaaggtaac 240
 acccatcaca aacgaggtgt gagcaaaactt ttcgtcgaat ttgtccaaca atttaataa 300
 attatcacta tctttggctt gcatgccaga ccaatcaatc atgacacatc cgaaaccata 360
 acgagtcata agatcaactg tgctaacaac aaacgtttcc cgataatgtt ctaccgctgc 420
 agtcttgga aattgatcgg acatagtcga accaccgacg gcgatcatgg ctttggcggtt 480
 gcccttatgt tgtgtaaaat gttccatata 510

<210> 46

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 Primer

<220>

<223> At location 15, n = a, c t or g

<400> 46
gaaccaaaaa chgtntgyta ytayg

25

<210> 47
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 47
gtaaaacgac ggccagt

17

<210> 48
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 48
gatatggaac atttyachca acayaargg

29

<210> 49
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 49
gtaatacgac tcactatagg gc

22

<210> 50
<211> 1445
<212> DNA
<213> Dermatophagoides farinae

<220>

<221> CDS

<222> (14)..(1399)

<400> 50

atcccaaata aaa atg act cga ttc tct ttg act gta ttg gcc gta ctt 49

Met Thr Arg Phe Ser Leu Thr Val Leu Ala Val Leu

1

5

10

gcc gct tgt ttc ggt tca aat att cgt ccg aat gtg gca act ttg gaa 97

Ala Ala Cys Phe Gly Ser Asn Ile Arg Pro Asn Val Ala Thr Leu Glu

15

20

25

cct aaa act gta tgt tac tat gaa tct tgg gta cat tgg cgc caa ggt 145

Pro Lys Thr Val Cys Tyr Tyr Glu Ser Trp Val His Trp Arg Gln Gly

30

35

40

gaa ggc aaa atg gat ccc gaa gac ata gat aca tcg ttg tgt act cac 193

Glu Gly Lys Met Asp Pro Glu Asp Ile Asp Thr Ser Leu Cys Thr His

45

50

55

60

att gtc tac tct tat ttc ggc att gat gct gcc act cat gag att aaa 241

Ile Val Tyr Ser Tyr Phe Gly Ile Asp Ala Ala Thr His Glu Ile Lys

65

70

75

cta ttg gat gaa tat ctt atg aaa gat tta cat gac atg gaa cat ttc 289

Leu Leu Asp Glu Tyr Leu Met Lys Asp Leu His Asp Met Glu His Phe

80

85

90

acg cag cat aag ggc aac gcc aaa gcc atg atc gcc gtc ggt ggt tcg 337

Thr Gln His Lys Gly Asn Ala Lys Ala Met Ile Ala Val Gly Gly Ser

95

100

105

act atg tcc gat caa ttt tcc aag act gca gcg gta gaa cat tat cgg 385

Thr Met Ser Asp Gln Phe Ser Lys Thr Ala Ala Val Glu His Tyr Arg

110

115

120

gaa acg ttt gtt gtt agc aca gtt gat ctt atg act cgt tat ggt ttc 433

Glu Thr Phe Val Val Ser Thr Val Asp Leu Met Thr Arg Tyr Gly Phe

125

130

135

140

gat ggt gtc atg att gat tgg tct ggc atg caa gcc aaa gat agt gat 481

Asp Gly Val Met Ile Asp Trp Ser Gly Met Gln Ala Lys Asp Ser Asp

145

150

155

aat ttc att aaa ttg ttg gac aaa ttc gac gaa aag ttt gct cac acc 529

Asn Phe Ile Lys Leu Leu Asp Lys Phe Asp Glu Lys Phe Ala His Thr

160

165

170

001160-2629960

| | |
|---|------|
| tcg ttt gtg atg ggt gtt acc ttg ccg gca acg atc gca tca tac gat | 577 |
| Ser Phe Val Met Gly Val Thr Leu Pro Ala Thr Ile Ala Ser Tyr Asp | |
| 175 180 185 | |
| aac tat aac att cct gcc atc tcc aac tat gtc gat ttt atg aac gtg | 625 |
| Asn Tyr Asn Ile Pro Ala Ile Ser Asn Tyr Val Asp Phe Met Asn Val | |
| 190 195 200 | |
| ctt agt ctg gat tac act gga tca tgg gcc cat acg gtc ggt cat gct | 673 |
| Leu Ser Leu Asp Tyr Thr Gly Ser Trp Ala His Thr Val Gly His Ala | |
| 205 210 215 220 | |
| tct ccg ttt cct gaa caa ctc aaa acg cta gaa gct tac cac aaa cga | 721 |
| Ser Pro Phe Pro Glu Gln Leu Lys Thr Leu Glu Ala Tyr His Lys Arg | |
| 225 230 235 | |
| ggc gct cca cgt cat aag atg gtc atg gct gta cca ttt tat gca cgt | 769 |
| Gly Ala Pro Arg His Lys Met Val Met Ala Val Pro Phe Tyr Ala Arg | |
| 240 245 250 | |
| acc tgg att ctc gag aaa atg aac aaa cag gac att ggc gat aaa gct | 817 |
| Thr Trp Ile Leu Glu Lys Met Asn Lys Gln Asp Ile Gly Asp Lys Ala | |
| 255 260 265 | |
| agt gga cca ggc cca cga ggt cag ttt aca cag act gat ggt ttc ctt | 865 |
| Ser Gly Pro Gly Pro Arg Gly Gln Phe Thr Gln Thr Asp Gly Phe Leu | |
| 270 275 280 | |
| agc tac aac gaa ttg tgc gtt cag att cag gcc gaa acg aat gca ttc | 913 |
| Ser Tyr Asn Glu Leu Cys Val Gln Ile Gln Ala Glu Thr Asn Ala Phe | |
| 285 290 295 300 | |
| acc att act cgt gat cat gat aat acc gca att tac gct gtc tat gtg | 961 |
| Thr Ile Thr Arg Asp His Asp Asn Thr Ala Ile Tyr Ala Val Tyr Val | |
| 305 310 315 | |
| cat agc aac cat gca gaa tgg atc tct ttc gaa gac cga cat aca ctt | 1009 |
| His Ser Asn His Ala Glu Trp Ile Ser Phe Glu Asp Arg His Thr Leu | |
| 320 325 330 | |
| ggc gaa aaa gca aaa aac ata acc caa caa gga tat gct gga atg tca | 1057 |
| Gly Glu Lys Ala Lys Asn Ile Thr Gln Gln Gly Tyr Ala Gly Met Ser | |
| 335 340 345 | |
| gtc tac aca ttg tcc aac gaa gat gtg cac ggc gtt tgt ggt gat aaa | 1105 |
| Val Tyr Thr Leu Ser Asn Glu Asp Val His Gly Val Cys Gly Asp Lys | |
| 350 355 360 | |

aac cct ttg ttg cat gct atc caa tcg aac tat tat cat ggc gtg gta 1153
 Asn Pro Leu Leu His Ala Ile Gln Ser Asn Tyr Tyr His Gly Val Val
 365 370 375 380

acc gaa ccg acc gtc gtt aca ctt cct cca gtc aca cat aca aca gaa 1201
 Thr Glu Pro Thr Val Val Thr Leu Pro Pro Val Thr His Thr Thr Glu
 385 390 395

cat gtg acc gat ata cca ggc gtg ttt cat tgc cat gaa gaa gga ttc 1249
 His Val Thr Asp Ile Pro Gly Val Phe His Cys His Glu Glu Gly Phe
 400 405 410

ttc cgc gat aag acc tat tgt gcc aca tac tac gaa tgc aaa aaa ggc 1297
 Phe Arg Asp Lys Thr Tyr Cys Ala Thr Tyr Tyr Glu Cys Lys Lys Gly
 415 420 425

gat ttt gga ctg gag aaa acc gtg cat cat tgt gcc aat cac tta cag 1345
 Asp Phe Gly Leu Glu Lys Thr Val His His Cys Ala Asn His Leu Gln
 430 435 440

gca ttt gac gaa gta agt cgg aca tgt att gat cat acc aaa ata ccc 1393
 Ala Phe Asp Glu Val Ser Arg Thr Cys Ile Asp His Thr Lys Ile Pro
 445 450 455 460

ggc tgt tgaatacaaa taaaattaca atcactttaa aaaaaaaaaa aaaaaa 1445
 Gly Cys

<210> 51
 <211> 462
 <212> PRT
 <213> Dermatophagoides farinae

<400> 51
 Met Thr Arg Phe Ser Leu Thr Val Leu Ala Val Leu Ala Ala Cys Phe
 1 5 10 15

Gly Ser Asn Ile Arg Pro Asn Val Ala Thr Leu Glu Pro Lys Thr Val
 20 25 30

Cys Tyr Tyr Glu Ser Trp Val His Trp Arg Gln Gly Glu Gly Lys Met
 35 40 45

Asp Pro Glu Asp Ile Asp Thr Ser Leu Cys Thr His Ile Val Tyr Ser
 50 55 60

Tyr Phe Gly Ile Asp Ala Ala Thr His Glu Ile Lys Leu Leu Asp Glu

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240

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270

285

300

320

Ala Glu Trp Ile Ser Phe Glu Asp Arg His Thr Leu Gly Glu Lys Ala

325

330

335

Lys Asn Ile Thr Gln Gln Gly Tyr Ala Gly Met Ser Val Tyr Thr Leu
340 345 350

Ser Asn Glu Asp Val His Gly Val Cys Gly Asp Lys Asn Pro Leu Leu
355 360 365

His Ala Ile Gln Ser Asn Tyr Tyr His Gly Val Val Thr Glu Pro Thr
370 375 380

Val Val Thr Leu Pro Pro Val Thr His Thr Thr Glu His Val Thr Asp
385 390 395 400

Ile Pro Gly Val Phe His Cys His Glu Glu Gly Phe Phe Arg Asp Lys
405 410 415

Thr Tyr Cys Ala Thr Tyr Tyr Glu Cys Lys Lys Gly Asp Phe Gly Leu
420 425 430

Glu Lys Thr Val His His Cys Ala Asn His Leu Gln Ala Phe Asp Glu
435 440 445

Val Ser Arg Thr Cys Ile Asp His Thr Lys Ile Pro Gly Cys
450 455 460

<210> 52

<211> 1445

<212> DNA

<213> Dermatophagoides farinae

<400> 52

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gatgcacggg tttctccagt ccaaaatcgc cttttttgca ttcgtagtat gtggcacaat 180
aggtcttata gcggaagaat ccttcttcat ggcaatgaaa cagcctggg atatcgggtca 240
catgttctgt tgtatgtgtg actggaggaa gtgtaacgac ggtcgggttcg gttaccacgc 300
catgataata gttcgattgg atagcatgca acaaagggtt tttatcacca caaacgccgt 360
gcacatcttc gttggacaat gtgtagactg acattccagc atatccttgt tgggttatgt 420
tttttgcttt ttcaccaagt gtatgtcggg cttcgaaaga gatccattct gcatggttgc 480
tatgcacata gacagcgtaa attgcgggtat tatcatgata acgagtaatg gtgaatgcat 540
tcgtttcggc ctgaatctga acgcacaatt cgttgtagct aaggaaacca tcagtctgtg 600
taaactgacc tcgtgggcct ggtccactag ctttatcgcc aatgtcctgt ttgttcattt 660
tctcgagaat ccaggtagct gcataaaatg gtacagccat gaccatctta tgacgtggag 720
cgcctcgttt gtggtaagct tctagcgttt tgagttgttc aggaaacgga gaagcatgac 780
cgaccgtatg ggcccatgat ccagtgtaat ccagactaag cacgttcata aaatcgacat 840

agttggagat ggcaggaatg ttatagttat cgtatgatgc gatcgttgcc ggcaaggtaa 900
 caccatcac aaacgaggtg tgagcaaaact tttcgtcgaa tttgtccaac aatttaata 960
 aattatcact atcttttggt tgcattgccag accaatcaat catgacacca tcgaaacat 1020
 aacgagtcatt aagatcaact gtgctaacaa caaacgtttc ccgataatgt tctaccgctg 1080
 cagtcttgga aaattgatcg gacatagtcg aaccaccgac ggcgatcatg gctttggcgt 1140
 tgcccttatg ctgcgtgaaa tgttccatgt catgtaaatc tttcataaga tattcatcca 1200
 atagttaaata ctcatgagtg gcagcatcaa tgccgaaata agagtagaca atgtgagtac 1260
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 aagattcata gtaacatata gttttagggt ccaaagttgc cacattcgga cgaatatttg 1380
 aaccgaaaca agcggcaagt acggccaata cagtcaaaga gaatcgagtc atttttattt 1440
 gggat 1445

<210> 53

<211> 1386

<212> DNA

<213> *Dermatophagoides farinae*

<400> 53

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 tggcgccaag gtgaaggcaa aatggatccc gaagacatag atacatcggt gtgtactcac 180
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 gccatgatcg ccgtcggtgg ttcgactatg tccgatcaat tttccaagac tgcagcggta 360
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 ccggcaacga tcgcatcata cgataactat aacattcctg ccatctccaa ctatgtcgat 600
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 cataagatgg tcatggctgt accattttat gcacgtacct ggattctcga gaaaatgaac 780
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 gatggtttcc ttagctacaa cgaattgtgc gttcagattc aggccgaaac gaatgcattc 900
 accattactc gtgatcatga taataaccga atttacgctg tctatgtgca tagcaaccat 960
 gcagaatgga tctctttcga agaccgacat acacttggtg aaaaagcaaa aaacataacc 1020
 caacaaggat atgctggaat gtcagtctac acattgtcca acgaagatgt gcacggcgtt 1080
 tgtggtgata aaaacccttt gttgcatgct atccaatcga actattatca tggcgtggta 1140
 accgaaccga ccgtcggttac acttccctcca gtcacacata caacagaaca tgtgaccgat 1200
 ataccaggcg tgtttcattg ccatgaagaa ggattcttcc gcgataagac ctattgtgcc 1260
 acatactacg aatgcaaaaa aggcgatttt ggactggaga aaaccgtgca tcattgtgcc 1320
 aatcacttac aggcatttga cgaagtaagt cggacatgta ttgatcatac caaaataccc 1380
 ggttgt 1386

<210> 54

<211> 1386

<212> DNA

<213> Dermatophagoides farinae

<400> 54

acaaccgggt attttggtat gatcaataca tgtccgactt acttcgtcaa atgcctgtaa 60
gtgattggca caatgatgca cggttttctc cagtccaaaa tgcctttttt tgcattcgta 120
gtatgtggca caatagggtct tatcgcgga gaatccttct tcatggcaat gaaacacgcc 180
tggatatatcg gtcacatggt ctggttgatg tgtgactgga ggaagtgtaa cgacggtcgg 240
ttcggttacc acgccatgat aatagttcga ttggatagca tgcaacaaag ggttttttatc 300
accacaaacg ccgtgcacat cttcgttgga caatgtgtag actgacattc cagcatatcc 360
ttggttgggtt atgttttttg ctttttcacc aagtgtatgt cggctcttga aagagatcca 420
ttctgcatgg ttgctatgca catagacagc gtaaattgcy gtattatcat gatcacgagt 480
aatggtgaat gcattcgttt cggcctgaat ctgaacgcac aattcgttgt agctaaggaa 540
accatcagtc tgtgtaaact gacctcgtgg gcctgggtcca ctagctttat cgccaatgtc 600
ctggtttgttc attttctcga gaatccaggt acgtgcataa aatgggtacag ccatgaccat 660
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Arg Gln Gly Glu Gly Lys Met Asp Pro Glu Asp Ile Asp Thr Ser Leu
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tgt act cac att gtc tac tct tat ttc ggc att gat gct gcc act cat 144

| | | | | | | | | | | | | | | | | |
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| Asp | Lys | Ala | Ser | Gly | Pro | Gly | Pro | Arg | Gly | Gln | Phe | Thr | Gln | Thr | Asp | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| ggt | ttc | ctt | agc | tac | aac | gaa | ttg | tgc | gtt | cag | att | cag | gcc | gaa | acg | 816 |
| Gly | Phe | Leu | Ser | Tyr | Asn | Glu | Leu | Cys | Val | Gln | Ile | Gln | Ala | Glu | Thr | |
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| aat | gca | ttc | acc | att | act | cgt | gat | cat | gat | aat | acc | gca | att | tac | gct | 864 |
| Asn | Ala | Phe | Thr | Ile | Thr | Arg | Asp | His | Asp | Asn | Thr | Ala | Ile | Tyr | Ala | |
| | | | | 275 | | | | 280 | | | | | 285 | | | |
| gtc | tat | gtg | cat | agc | aac | cat | gca | gaa | tgg | atc | tct | ttc | gaa | gac | cga | 912 |
| Val | Tyr | Val | His | Ser | Asn | His | Ala | Glu | Trp | Ile | Ser | Phe | Glu | Asp | Arg | |
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| cat | aca | ctt | ggt | gaa | aaa | gca | aaa | aac | ata | acc | caa | caa | gga | tat | gct | 960 |
| His | Thr | Leu | Gly | Glu | Lys | Ala | Lys | Asn | Ile | Thr | Gln | Gln | Gly | Tyr | Ala | |
| 305 | | | | | | 310 | | | | | 315 | | | | 320 | |
| gga | atg | tca | gtc | tac | aca | ttg | tcc | aac | gaa | gat | gtg | cac | ggc | gtt | tgt | 1008 |
| Gly | Met | Ser | Val | Tyr | Thr | Leu | Ser | Asn | Glu | Asp | Val | His | Gly | Val | Cys | |
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| Gly | Asp | Lys | Asn | Pro | Leu | Leu | His | Ala | Ile | Gln | Ser | Asn | Tyr | Tyr | His | |
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| Gly | Val | Val | Thr | Glu | Pro | Thr | Val | Val | Thr | Leu | Pro | Pro | Val | Thr | His | |
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| aca | aca | gaa | cat | gtg | acc | gat | ata | cca | ggc | gtg | ttt | cat | tgc | cat | gaa | 1152 |
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| Glu | Gly | Phe | Phe | Arg | Asp | Lys | Thr | Tyr | Cys | Ala | Thr | Tyr | Tyr | Glu | Cys | |
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| Lys | Lys | Gly | Asp | Phe | Gly | Leu | Glu | Lys | Thr | Val | His | | | | | |
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SECRET

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Glu Ile Lys Leu Leu Asp Glu Tyr Leu Met Lys Asp Leu His Asp Met
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Glu His Phe Thr Gln His Lys Gly Asn Ala Lys Ala Met Ile Ala Val
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Gly Gly Ser Thr Met Ser Asp Gln Phe Ser Lys Thr Ala Ala Val Glu
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His Tyr Arg Glu Thr Phe Val Val Ser Thr Val Asp Leu Met Thr Arg
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Tyr Gly Phe Asp Gly Val Met Ile Asp Trp Ser Gly Met Gln Ala Lys
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Asp Ser Asp Asn Phe Ile Lys Leu Leu Asp Lys Phe Asp Glu Lys Phe
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Ser Tyr Asp Asn Tyr Asn Ile Pro Ala Ile Ser Asn Tyr Val Asp Phe
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Met Asn Val Leu Ser Leu Asp Tyr Thr Gly Ser Trp Ala His Thr Val
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His Lys Arg Gly Ala Pro Arg His Lys Met Val Met Ala Val Pro Phe
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Gly Phe Leu Ser Tyr Asn Glu Leu Cys Val Gln Ile Gln Ala Glu Thr
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Asn Ala Phe Thr Ile Thr Arg Asp His Asp Asn Thr Ala Ile Tyr Ala
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Val Tyr Val His Ser Asn His Ala Glu Trp Ile Ser Phe Glu Asp Arg
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His Thr Leu Gly Glu Lys Ala Lys Asn Ile Thr Gln Gln Gly Tyr Ala
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Gly Met Ser Val Tyr Thr Leu Ser Asn Glu Asp Val His Gly Val Cys
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